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Access DB# 104293
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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: BENNETT CELSA Examiner #: 73815 Date: 9/23/03
Art Unit: 1639 Phone Number 305-7556 Serial Number: 091848, 798
Mail Box and Bldg/Room Location: EM1 3B01 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Rh(D)- binding proteins —

Inventors (please provide full names): DONALD L. SIEGEL

Earliest Priority Filing Date: 5/27/97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

PLEASE SEARCH

1) SEQ ID ^{NA} 97-393 (cDNA)

2) SEQ ID ^{AA} 28-131 (protein; anti-Rh(D) chain E03)

IN

ALL RELEVANT DATABASES

— provide at least 20 hits which
"comprise" these sequences.

thanks

EXCELST

see attached BIB + claims (11-13, 22-37)

STAFF USE ONLY

Searcher: _____
Searcher Phone #: _____
Searcher Location: _____
Date Searcher Picked Up: 9/23
Date Completed: 9/25
Searcher Prep & Review Time: 12
Clerical Prep Time: _____
Online Time: 12

Type of Search

NA Sequence (#) 1
AA Sequence (#) 1
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr.Link _____
Lexis/Nexis _____
Sequence Systems CS
WWW/Internet _____
Other (specify) _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2003, 04:42:55 ; Search time 71 Seconds
(Without alignments)
292.862 Million cell updates/sec

Title: US-09-848-798a-28
Perfect score: 689
Sequence: 1 EVQLLESGVSGGGLVKPGC.....WVRSDGMVWGCGTTIVSS 131

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	689	100.0	131	22	AAAG93585	Human anti-Rh(D) c
2	643	93.3	127	22	AAAG93584	Human anti-Rh(D) c
3	511.5	74.2	256	23	ABP45307	Human BLYS binding
4	509	73.9	248	23	ABP44902	Human BLYS binding
5	507.5	73.7	245	20	AAV06717	Antibody 12B5 sing
6	506.5	73.5	247	23	ABP45753	Human BLYS binding
7	504.5	73.2	116	23	AAE28870	Human KDR (VEGFR-2
8	504.5	73.2	116	24	ABJ26763	VEGF binding relat
9	499.5	72.5	116	23	AAE28873	Human KDR (VEGFR-2

10	499.5	72.5	116	24	ABJ26766	VEGF binding relat
11	499.5	72.5	249	23	ABP45845	Human BLYS binding
12	499	72.4	125	23	ABG77142	Anti-IGF-IR antibo
13	498	72.3	241	23	ABP45926	Human BLYS binding
14	497.5	72.2	247	23	ABP45692	Human BLYS binding
15	496.5	72.1	473	23	ABG77162	Germline protein s
16	495.5	71.9	152	22	AAAB9911	Human protein SEO
17	495.5	71.9	249	23	ABP44963	Human BLYS binding
18	494.5	71.8	248	23	ABP45963	Human BLYS binding
19	493.5	71.6	262	23	ABP46070	Human BLYS binding
20	492.5	71.5	252	23	ABP45623	Human BLYS binding
21	491.5	71.3	128	22	AAE07014	Human heavy chain
22	491	71.3	250	23	ABP45168	Human BLYS binding
23	491	71.3	255	23	ABP45597	Human BLYS binding
24	490.5	71.2	124	23	AAO18439	Anti-GD2 antibody
25	489.5	71.0	248	23	ABP45954	Human BLYS binding
26	489	71.0	244	23	ABP45980	Human BLYS binding
27	488.5	70.9	125	22	AAAB2746	Human HIV-1 monocl
28	487.5	70.8	256	23	ABP45198	Human BLYS binding
29	487.5	70.8	258	23	ABP45830	Human BLYS binding
30	486	70.5	121	24	ABP56504	Human anti-FC-epsi
31	486	70.5	121	24	ABP56506	Human anti-FC-epsi
32	485.5	70.5	250	23	ABP45602	Human BLYS binding
33	485	70.4	173	22	AAE07024	Human heavy chain
34	485	70.4	173	20	AAV34306	IGG antibody 2.1.1
35	484	70.2	255	23	ABP45808	Human BLYS binding
36	484	70.2	470	23	ABG77158	Germline protein s
37	483	70.1	121	22	AAE07029	Human heavy chain
38	483	70.1	121	24	ABP56507	Human anti-FC-epsi
39	483	70.1	125	22	AAE07013	Human heavy chain
40	483	70.1	127	22	AAU02616	Anti-adipocyte mon
41	483	70.1	556	20	AAW00218	Bispecific tetra
42	482.5	70.0	124	20	AAW00285	Human anti-Grp78/I
43	482.5	70.0	252	23	ABP45351	Human BLYS binding
44	482.5	70.0	253	24	ABJ19830	Human VEGF-2 relat
45	481	69.8	123	18	AAW08582	Human antibody C4.

ALIGNMENTS

RESULT 1	
AAAG3585	
ID	AAAG3585 standard; Protein; 131 AA.
XX	
AC	AAAG3585;
XX	
DT	14-SEP-2001 (first entry)
XX	
DE	Human anti-Rh(D) chain E03 protein sequence.
XX	
KW	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW	red blood cell; Rh phenotype; diagnosis; therapeutic.
XX	
OS	Homo sapiens.
XX	
PN	US6255455-B1.
XX	
PD	03-JUL-2001.
XX	
PF	29-JAN-1999; 99US-0240274.
XX	
PR	11-OCT-1996; 96US-0028550.
PR	10-APR-1998; 98US-0081380.
PR	27-JUN-1997; 97US-0884045.
XX	
PA	(USPE-) UNIV PENNSYLVANIA.
XX	
PI	Siegel DL;
XX	
DR	WPI; 2001-388931/41.
DR	N-PSDB; AAH68642.
XX	

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -

PS Claim 1; Column 43; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

CC Sequence 131 AA:

Query Match 100.0%; Score 689; DB 22; Length 131;

Best Local Similarity 100.0%; Pred. No. 9, 1e-55; Mismatches 0; Indels 0; Gaps 0;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLLESGYVESGGGLYKPGGSLRLSCAASGFTFSYSMHWYRQPGKGLVYSINSNT 60

DB 1 EVQLLESGYVESGGGLYKPGGSLRLSCAASGFTFSYSMHWYRQPGKGLVYSINSNT 60

QY 61 YIYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSTRYSNFLRWVRSDGMV 120

DB 61 YIYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSTRYSNFLRWVRSDGMV 120

QY 121 WGQGTIVIVSS 131

DB 121 WGQGTIVIVSS 131

RESULT 2

AAG93584

ID AAG93584 standard; Protein; 127 AA.

AC AAG93584;

DE 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain E01s protein sequence.

KW Human: anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

XX red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US625455-B1.

PD 03-JUL-2001.

PE 29-JAN-1999; 99US-0240274.

PR 11-OCT-1996; 96US-0028550.

PR 10-APR-1998; 98US-0081380.

PR 27-JUN-1997; 97US-0884045.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

XX WPI; 2001-388931/41.

DR N-PSDB; AAH68641.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -

PS Claim 1; Column 43; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

CC Sequence 127 AA:

Query Match 93.3%; Score 643; DB 22; Length 127;

Best Local Similarity 95.4%; Pred. No. 1, 3e-50; Mismatches 2; Indels 4; Gaps 1;

Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 EVQLLESGYVESGGGLYKPGGSLRLSCAASGFTFSYSMHWYRQPGKGLVYSINSNT 60

DB 1 EVQLLESGYVESGGGLYKPGGSLRLSCAASGFTFSYSMHWYRQPGKGLVYSINSNT 56

QY 61 YIYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSTRYSNFLRWVRSDGMV 120

DB 57 YIYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSTRYSNFLRWVRSDGMV 116

QY 121 WGQGTIVIVSS 131

DB 117 WGQGTIVIVSS 127

RESULT 3

ABP45307

ID ABP45307 standard; Protein; 256 AA.

AC ABP45307;

DE 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1318.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PE 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

DR Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -

XX PS Claim 1; Page 1975-1976; 3148bp; English.
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 XX CC tumor necrosis factor (TNF) super family and induces B cell
 XX CC proliferation and differentiation. The antibodies of the invention have
 XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
 XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX CC and so may be used to detect and quantitate the presence of Blys in
 XX CC biological samples and may be used in this way to diagnose disease
 XX CC associated with aberrant expression of Blys. They may also be
 XX CC administered to treat diseases associated with aberrant Blys expression
 XX CC and activity such as cancer, immune, and autoimmune disorders and
 XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX CC the antibodies and fragments of the antibodies described in the method
 XX CC of the invention.
 XX SQ Sequence 256 AA;
 Query Match 74.2%; Score 511.5; DB 23; Length 256;
 Best Local Similarity 78.2%; Pred. No. 2.1e-38;
 Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;
 OY 1 EVOLLESGVESGGGLVPRGGSRLRSCAASGFFFSYSHMWVRQGGKLEWVSSISNSNT 60
 DB 1 EVOL---VQSGGGLVPRGGSRLRSCAASGFFFSYSHMWVRQAGKLEWVSSISNS 56
 OY 61 YYYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARD-SRYSNLEWVSD--G 117
 DB 57 YYYADSVKGRFTISRDNKNSLYLQMSLRAEDRAVYYCARDLGFIDLALALENG 116
 OY 118 MDVWGQGTIVYVS 130
 DB 117 MDVWGKGLVTVYS 129
 RESULT 4
 ABP44902 ID ABP44902 standard; Protein; 248 AA.
 AC ABP44902;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scfv SEQ ID 913.
 XX KW Blys: B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 XX KW antiAIDS; vaccine; cancer; autoimmune disorder; immunodeficiency;
 XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX PA (HUMA-) HUMAN GENOME SCT INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX DR WPI; 2002-114799/15.
 XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for
 XX PT the diagnosis and treatment of cancers and immune disorders -
 XX PS Claim 1; Page 1491-1492; 3148bp; English.
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 XX CC tumor necrosis factor (TNF) super family and induces B cell
 XX CC proliferation and differentiation. The antibodies of the invention have
 XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
 XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX CC and so may be used to detect and quantitate the presence of Blys in
 XX CC biological samples and may be used in this way to diagnose disease
 XX CC associated with aberrant expression of Blys. They may also be
 XX CC administered to treat diseases associated with aberrant Blys expression
 XX CC and activity such as cancer, immune, and autoimmune disorders and
 XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX CC the antibodies and fragments of the antibodies described in the method
 XX CC of the invention.
 XX SQ Sequence 248 AA;
 Query Match 73.9%; Score 509; DB 23; Length 248;
 Best Local Similarity 78.6%; Pred. No. 3.4e-38;
 Matches 103; Conservative 8; Mismatches 14; Indels 6; Gaps 2;
 OY 1 EVOLLESGVESGGGLVPRGGSRLRSCAASGFFFSYSHMWVRQGGKLEWVSSISNSNT 60
 DB 1 EVOL---VESGGGLVPRGGSRLRSCAAGFFFSYSHMWVRQAGKLEWVSSISNRS 56
 OY 61 YYYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSDRYSNLEWVRSGM 120
 DB 57 YYYADSVKGRFTISRDNKNSLYLQMSLRAEDRAVYYCARDGR--DILTVYYGGLDV 114
 OY 121 WGQGTIVYVS 131
 DB 115 WGQGLTVYVS 125
 RESULT 5
 AAY06717 ID AAY06717 standard; Protein; 245 AA.
 XX AC AAY06717;
 XX DT 17-JUN-1999 (first entry)
 XX DE Antibody 12B5 single chain Fv (scfv) fragment.
 XX KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
 XX KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
 XX KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
 XX KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MusK; CDR;
 XX KW neuromuscular; muscular dystrophy; complementarity determining region.
 XX OS Homo sapiens.
 XX PN WO9910494-A2.
 XX PD 04-MAR-1999.
 XX FT Key Location/Qualifiers
 XX FT Misc-difference 208
 XX FT /note="unspecified"

PF 21-AUG-1998; 98WO-US17364.
 XX 25-AUG-1997; 97US-0918148.
 PR (GETH) GENENTECH INC.
 XX
 XX Adams CW, Carter PJ, Fendly BM, Gurney AL;
 PI WPI: 1999-204666/17.
 DR New thrombopoietin receptor agonist antibodies - useful for
 PT treating immunological or hematological disorders
 XX
 XX Disclosure; Fig 1; 86pp; English.
 XX The invention relates to an agonist antibody (Ab) which binds to a
 CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
 CC be used in the same way and for the same indications as thrombopoietin
 CC (TPO). They can stimulate proliferation, differentiation or growth of
 CC megakaryocytes. They may also be able to stimulate megakaryocytes to
 CC increase platelet production. They can be used for treating
 CC immunological or hematopoietic disorders, especially thrombocytopenia.
 CC Thrombocytopenia - associated bone marrow hypoplasia (e.g. aplastic anemia
 CC following chemotherapy or bone marrow transplant) may be effectively
 CC treated with the antibody compounds as well as disorders such as
 CC disseminated intravascular coagulation (DIC), immune thrombocytopenia,
 CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
 CC congenital thrombocytopenia, thrombotic thrombocytopenia and
 CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
 CC treatment of solid tumours or leukemia, myeloblastic chemotherapy for
 CC autologous or allogeneic bone marrow transplant, myelodysplasia,
 CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
 CC thrombocytopenia. The antibodies which bind to the TPO-R receptor can be
 CC used for improving neuromuscular function in a patient, e.g. in muscular
 CC dystrophy. The products can also be used for detection and diagnosis. The
 CC antibodies have a longer half-life than the natural ligand for the TPO-R.
 CC Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
 CC various antibodies.
 CC
 XX Sequence 245 AA;
 SQ
 Query Match 73.7%; Score 507.5; DB 20; Length 245;
 Best Local Similarity 77.9%; Pred. No. 4.6e-38;
 Matches 102; Conservative 9; Mismatches 7; Indels 13; Gaps 2;
 QY 1 EVOLLESYVESGGGLVKGPGSLRLSCAASGFTFSYSMHWVQGGKLEWVSSISNSNT 60
 Db 3 QVQL---VESGGGLVKGPGSLRLSCAASGFTFSYSHNMWVQAGKLEWVSSISSSSS 58
 QY 61 YYYADAVKGRFTISDNKNSLYLQMSLRAEHRAVYVCARDSRYSNFLRWVSGDMV 120
 Db 59 YYYADSVKGRFTISDNKNSLYLQMSLRAEDRAVYVCARDR-----GSTGMDV 109
 QY 121 WGOGTVIVSS 131
 Db 110 WGRGTLVTVSS 120
 RESULT 6
 ID ABA45753 standard; Protein: 247 AA.
 AC ABA45753;
 XX
 XX 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 1764.
 XX
 XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antiinflammatory;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
 PD
 XX 15-JUN-2001; 2001WO-US19110.
 PF 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI: 2002-114799/15.
 DR
 XX
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 2507-2508; 3148pp; English.
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antiinflammatory and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABA43990-ABA47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 CC
 XX Sequence 247 AA;
 SQ
 Query Match 73.5%; Score 506.5; DB 23; Length 247;
 Best Local Similarity 78.6%; Pred. No. 5.7e-38;
 Matches 103; Conservative 10; Mismatches 11; Indels 7; Gaps 3;
 QY 1 EVOLLESYVESGGGLVKGPGSLRLSCAASGFTFSYSMHWVQGGKLEWVSSISNSNT 60
 Db 1 QVQL---VQSGGGLVKGPGSLRLSCAASGFTFSYSHNMWVQAGKLEWVSSISSSSS 56
 QY 61 YYYADAVKGRFTISDNKNSLYLQMSLRAEHRAVYVCARDSRYSNFLRWVSGDMV 120
 Db 57 YYYADSVKGRFTISDNKNSLYLQMSLRAEDRAVYVCARD-EDYILGLGLQ--CMDV 113
 QY 121 WGOGTVIVSS 131
 Db 114 WGRGTLVTVSS 124
 RESULT 7
 ID AAE28870 standard; Protein: 116 AA.
 AC AAE28870;
 XX
 XX 27-DEC-2002 (first entry)
 DE
 XX

DE Human KDR (VEGFR-2) Fab heavy chain protein from D2C6 and D1H4 clone.
KW Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
OS Homo sapiens.
PN WO200270008-A1.
PN 12-SEP-2002.
PD 04-MAR-2002; 2002WO-US06762.
PF 02-MAR-2001; 2001US-0796889.
PR (IMCL-) IMCLONE SYSTEMS INC.
PA (ROCK) ROCKWELL P.
PA (GOLD) GOLDSTEIN N I.
XX WPI; 2002-691738/74.
DR N-PSDB: AAD46290, AAD46292.
XX
XX
PT Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists -
PS
PS Example 9; Page 123; 151pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC preferably high vascular tumours and non-solid tumours. The inhibition
CC or reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours,
CC where the progression of tumours includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human KDR (VEGFR-2) Fab antibody heavy chain protein.
XX
XX Sequence 116 AA;
XQ

[illegible]

DT	01-MAY-2003	(first entry)
DE	VEGF binding related protein SEQ ID NO 76.	
KX	Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;	
KW	leukemia cell; vascular endothelial growth factor; tumour;	
KM	bispecific antigen-binding protein; human.	
OS	Homo sapiens.	
PN	WO200302144-A1.	
PD	09-JAN-2003.	
PF	26-JUN-2002; 2002WO-US20332.	
PR	26-JUN-2001; 2001US-301299P.	
PA	(IMCL-) IMCLONE SYSTEMS INC.	
PI	Zhu Z:	
DR	WPI: 2003-201468/19.	
N-PSDB	ABT23325.	
PT	New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -	
PS	Claim 15; page 70-71; 98pp; English.	
CC	The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor. A second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukemia cells. The antibodies are useful for treating tumors and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a human protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.	
SQ	Sequence 116 AA;	
Query Match	73.2%; Score 504.5; DB 24; Length 116;	
Best Local Similarity	77.1% Pred. No. 3.8e-38;	
Matches 101; Conservative	8; Mismatches 7; Indels 15; Gaps 2;	

QY		EVOLLESGVEGEGGLVPGGSLRLSCAASGFTFSYSMHWVRGGKGLEWVSSTSNNT	60
		1 EVOL-----VSGGGGLVPGGSLRLSCAASGFTFSYSNMWRQAPKGLEWVSSTSSSSS	56
Dd			
QY		61 YIYYADAVKGFRTISRDNAKNSLYLNQNLSLAETHTAVYYCARDSRYSNFLRWVRSDGMIV	120
		57 YIYYADSVKGRFRTISRDNAKNSLYLNQNLSLAEDPTAVYYCAR-----VTDAADI	105
QY		121 WGCGTIVIVSS 131	
Dd		106 WGCGTIVTVVSS 116	
RESULT 9			
AAE28873			
ID	AAE28873	standard; Protein; 116 AA.	
XX			
AC	AAE28873:		
XX			
DT	27-DEC-2002	(first entry)	
XX			
DE	Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.		
XW	Human; tumour; vascular endothelial growth factor receptor; metastasis;		

KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KM breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
 XX Homo sapiens.
 OS
 PN WO200270008-A1.
 PD 12-SEP-2002.
 PF 04-MAR-2002; 2002WO-US06762.
 PR 02-MAR-2001; 2001US-0798689.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 XX
 DR WPI: 2002-691738/74.
 DR N-PSDB; AAD46294.
 XX
 PT Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists -
 PS Example 12; Page 127; 151pp; English.
 XX
 PS The invention relates to a method of inhibiting tumor growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumor growth in a human, where the tumor (e.g.,
 CC tumor of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumor
 CC or non-small cell lung carcinoma (NSCLC) and tumor overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumors,
 CC preferably high vascular tumors and non-solid tumors. The inhibition
 CC or progression of tumor growth includes prevention or inhibition of the
 CC progression of tumor, including cancerous and non-cancerous tumors,
 CC where the progression of tumors includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumor. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain protein.
 CC
 SO Sequence 116 AA;
 Query Match 72.5%; Score 499.5; DB 23; Length 116;
 Best Local Similarity 76.3%; Pred. No. 1.1e-37;
 Matches 100; Conservative 9; Mismatches 7; Indels 15; Gaps 2;
 QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSSYMHVVRGQPGKGLWVSSISNSNT 60
 DB 1 EVOL----VOSGGGLVPGGSLRLSCAASGFTSSSYMHVVRGQPGKGLWVSSISNSNT 56
 QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYVCARDSRYSNPLRWVRSDGMV 120
 DB 57 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYVCAR-----VTDADF 105
 QY 121 WGCGTIVYSS 131
 DB 106 WGCGTIVYSS 116
 RESULT 10
 ID ABJ26766 standard; Protein: 116 AA.
 AC ABJ26766;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE VEGF binding related protein SEQ ID No 83.

XX
 KM Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KM leukaemia cell; vascular endothelial growth factor; tumour;
 KM bispecific antigen-binding protein; human.
 XX
 OS Homo sapiens.
 PN WO2003002144-A1.
 PD 09-JAN-2003.
 PF 26-JUN-2002; 2002WO-US20332.
 PR 26-JUN-2001; 2001US-301299P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA
 PI Zhu Z;
 PI
 DR WPI: 2003-201468/19.
 DR N-PSDB; ABT23330.
 XX
 PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a
 PT second VEGF receptor, useful for inhibiting migration of leukemia
 PT cells, or for treating tumors -
 PS Claim 15; Page 74; 98pp; English.
 XX
 PS The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells
 CC and migration of leukemia cells. The antibodies are useful for treating
 CC tumors and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a human protein relating to the
 CC bispecific antibodies that bind to the VEGF receptors of the invention.
 CC
 SO Sequence 116 AA;
 Query Match 72.5%; Score 499.5; DB 24; Length 116;
 Best Local Similarity 76.3%; Pred. No. 1.1e-37;
 Matches 100; Conservative 9; Mismatches 7; Indels 15; Gaps 2;
 QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSSYMHVVRGQPGKGLWVSSISNSNT 60
 DB 1 EVOL----VOSGGGLVPGGSLRLSCAASGFTSSSYMHVVRGQPGKGLWVSSISNSNT 56
 QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYVCARDSRYSNPLRWVRSDGMV 120
 DB 57 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYVCAR-----VTDADF 105
 QY 121 WGCGTIVYSS 131
 DB 106 WGCGTIVYSS 116
 RESULT 11
 ID ABP45845 standard; Protein: 249 AA.
 AC ABP45845;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1856.
 XX
 KM Blys: B lymphocyte stimulator; TNF superfamily; human; cytosstatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunomodulatory; antithematic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PM WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI: 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2616-2617; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 249 AA;
Query Match 72.5%; Score 499.5; DB 23; Length 249;
Best Local Similarity 78.6%; Pred. No. 2.5e-37;
Matches 103; Conservative 7; Mismatches 14; Indels 7; Gaps 3;
QY 1 EVQLLESGVSGGGLVPRGSLRLSCAASGFTFSYSHMWYRQPGKLEWVSISNT 60
DB 1 EVQL-----VESGGGVLPFGSLRLSCAASGFTFSYSHMWYRQPGKLEWVSISNT 56
QY 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLAHEHTAVYVCARDSRYSNLEWVRSDGMDV 120
DB 57 IITYYADSVKGRFTISRDNAKNSLYLQMNSLAHEHTAVYVCAR-GRYDILTGFTTS--FDY 113
QY 121 WGQGTIVVSS 131
DB 114 WGQGTIVVSS 124
RESULT 12
ABG77142
ID ABG77142 standard; Protein: 125 AA.
XX
AC ABG77142;
XX
DT 24-OCT-2002 (first entry)

XX
DE Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.
XX
XX Insulin-like growth factor I receptor; antibody; human;
KM cytosolic; osteopathic; antiatherosclerotic; antipsoriatic;
KM IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KM neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KM atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200253596-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-US51113.
XX
XX 05-JAN-2001; 2001US-259927P.
XX
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvajan JR, Gallo M;
XX
XX WPI: 2002-575410/61.
XX N-PSDB; ABS62704.
XX
XX Novel humanized, chimeric monoclonal antibody that specifically binds
XX to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
XX binding of IGF-I or IGF-II to receptor and for treating cancer in
XX humans -
XX
XX Claim 13; Page 130; 172pp; English.
XX
CC This invention relates to a novel humanised, chimeric or human
CC monoclonal antibody or its antigen binding portion that specifically
CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC phosphorylation. The antibodies of the invention are useful for
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC subject. The antibody or its antigen-binding portion is also useful for
CC treating cancer in a human. The method for this further involves an anti
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC The antibodies may also be useful for increasing IGF-IR activity and
CC thus restoring IGF-IR activity in a condition characterised by low
CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
CC invention is also useful for inducing apoptosis of specific cells in a
CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC antibodies minimise the immunogenic and allergic responses intrinsic to
CC mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC efficacy and safety of the administered antibodies. The present sequence
CC represents an anti-insulin-like growth factor I receptor antibody of the
CC invention.
XX
SQ Sequence 125 AA;
Query Match 72.4%; Score 499; DB 23; Length 125;
Best Local Similarity 76.3%; Pred. No. 1.3e-37;
Matches 100; Conservative 9; Mismatches 16; Indels 6; Gaps 2;
QY 1 EVQLLESGVSGGGLVPRGSLRLSCAASGFTFSYSHMWYRQPGKLEWVSISNT 60
DB 1 EVQL-----ESGGGVLPFGSLRLSCAASGFTFSYSHMWYRQPGKLEWVSISNT 56
QY 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLAHEHTAVYVCARDSRYSNLEWVRSDGMDV 120
DB 57 IITYYADSVKGRFTISRDNAKNSLYLQMNSLAHEHTAVYVCAR-KADYGDFYYYY--GMDV 114
QY 121 WGQGTIVVSS 131
DB 115 WGQGTIVVSS 125

```

RESULT 13
ID ABP45926
XX ABP45926 standard; protein; 241 AA..
AC
XX ABP45926;
DE
XX 19-AUG-2002 (first entry)
DE Human BlyS binding scFv SEQ ID 1937.
XX
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antithematic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001MO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277378P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PL Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR WPI: 2002-114799/15.
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
PS Claim 1; Page 2712-2713; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency, e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP45390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
Sequence 241 AA:
Query Match 72.3%; Score 498; DB 23; Length 241;
Best Local Similarity 77.7%; Pred. No. 3.3e-37;
Matches 101; Conservative 7; Mismatches 8; Indels 14; Gaps 2
OY 2 VOLLESGGAGGLVXPGGSRLRSCAAAGFTFFSSYSMHWWROGKGLEWVSINSNTY 61
||| 1-||||||| ||||||| ||||||| ||||||| :||| ||||||| ||||| :|||
Db 2 VOL-----VDSGGIVLXSGGSRLRSCAAAGFTFFSSYSNMWVROAKGLEWVSISSTSY 57

```

Oy		62	IYYADVKRFRITSRPNANKSLYLQMLNSLRHETVYVCASDSTRSNFLRWVRSDGMDWV	12
Xx				
Dd		58	IYYADVSKRKFRITSRNNAKNSLYLQLMNSLRADCTAVYCCAGHHY-----GMDWV	107
Oy		122	GOSTIYVSS	131
Xx				
Dd		108	GRGIWTVSS	117
RESULT 14				
ABP45692				
ID	ABP45692 standard; Protein; 247 AA.			
AC	ABP45692;			
DY	19-AUG-2002 (first entry)			
XX				
DE	Human Bly5 binding scFv SEQ ID 1703.			
KW	Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;			
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;			
KW	immunosuppressive; immunostimulant; immunomodulatory; antineumatic;			
KM	antiAIDS vaccine; cancer; immune; autoimmune disorder; immunodeficiency;			
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;			
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.			
OS	Homo sapiens.			
PX	WO200202641-A1.			
PN				
PD	10-JAN-2002.			
XX				
PF	15-JUN-2001; 2001WO-US91110.			
XX				
PR	16-JUN-2000; 2000US-212210P.			
PR	17-OCT-2000; 2000US-240816P.			
PR	16-MAR-2001; 2001US-246248P.			
PR	21-MAR-2001; 2001US-277359P.			
PR	23-MAY-2001; 2001US-293499P.			
PA	(HUMA-) HUMAN GENOME SCI INC.			
FA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.			
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;			
DR	WPI; 2002-114799/15.			
XX				
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for			
XX	the diagnosis and treatment of cancers and immune disorders -			
PS	Claim 1; Page 2434-2435; 3148bp; English.			
XX				
CC	This invention describes novel antibodies that immunospecifically bind to			
CC	B Lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the			
CC	tumour necrosis factor (TNF) super family and induces B cell			
CC	proliferation and differentiation. The antibodies of the invention have			
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,			
CC	antineumatic and antiAIDS activity and can be used in vaccines to			
CC	inhibit the expression and activity of Bly5. The antibodies bind to Bly5			
CC	and so may be used to detect and quantitate the presence of Bly5 in			
CC	biological samples and may be used in this way to diagnose disease			
CC	associated with aberrant expression of Bly5. They may also be			
CC	administered to treat diseases associated with aberrant Bly5 expression			
CC	and actively such as cancer, immune, and autoimmune disorders and			
CC	diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,			
CC	Immunodeficiency (e.g. common variable immunodeficiency CVID) and			
CC	acquired Immunodeficiency Syndrome (AIDS)). ABP43590-ABP47228 represent			
CC	of the antibodies and fragments of the antibodies described in the method			
XX				
SQ	Sequence 247 AA;			

Query Match 72.2%; Score 497.5; DB 23; Length 247;

Best Local Similarity 78.6%; Pred. No. 3.7e-37;
Matches 103; Conservative 8; Mismatches 13; Indels 7; Gaps 3;

QY 1 EVOLLESGVGGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
DB 1 QVQL---VESGGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNS 56
61 YIYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSRYSNFLRWSDGMDV 120
DB 57 YIYADSVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCA-TLGYIDILGYNSD--DY 113
QY 121 WGQGTIVIVSS 131
DB 114 WGKGLIVTVSS 124

RESULT 15
ABG77162
ID ABG77162 standard; Protein: 473 AA.
XX
AC ABG77162;
XX
DT 24-OCT-2002 (first entry)
XX
DE Germline protein sequence of anti-IGF-IR antibody DP-35(3-11)/D3-3/JH6.
XX
KW Insulin-like growth factor I receptor; antibody; human;
KW Cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KW atherosclerosis.
XX
OS Homo sapiens.
XX
PN W0200253596-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-US51113.
XX
PR 05-JAN-2001; 2001US-259927P.
XX
PA (PE12) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR WPL: 2002-575410/61.
XX
PT Novel humanized, chimeric monoclonal antibody that specifically binds
PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
PT binding of IGF-I or IGF-II to receptor and for treating cancer in
PT humans -
XX
PS Disclosure: Figure 19D; 172pp; English.
XX
CC This invention relates to a novel humanised, chimeric or human
CC monoclonal antibody or its antigen binding portion that specifically
CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC phosphorylation. The antibodies of the invention are useful for
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC subject. The antibody or its antigen-binding portion is also useful for
CC treating cancer in a human. The method for this further involves an anti
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC The antibodies may also be useful for increasing IGF-IR activity and
CC thus restoring IGF-IR activity in a condition characterised by low
CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
CC invention is also useful for inducing apoptosis of specific cells in a
CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC antibodies minimise the immunogenic and allergic responses intrinsic to

CC mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC efficacy and safety of the administered antibodies. The present sequence
CC represents an anti-insulin-like growth factor I receptor antibody of the
CC invention.

XX Sequence 473 AA;

Query Match 72.1%; Score 496.5; DB 23; Length 473;

Best Local Similarity 76.3%; Pred. No. 9.4e-37;
Matches 103; Conservative 6; Mismatches 15; Indels 11; Gaps 3;

QY 1 EVOLLESGVGGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
DB 20 QVQL---VESGGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNS 75
61 YIYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARDSRYSNFLRWSDGMDV 116
DB 76 YIYADSVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARVLR---FLEMLLYYYYYY 132
QY 117 GMDYWGQGTIVIVSS 131
DB 133 GMDYWGQGTIVTVSS 147

Search completed: September 24, 2003, 06:26:49
Job time : 72 secs

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OM protein - protein search, using sw model

Run on: September 24, 2003, 05:55:00 ; Search time 39 seconds

(without alignments)
323.028 Million cell updates/sec

Title: US-09-848-798a-28

Perfect score: 689
Sequence: 1 EVQLLESGVSGGGLVPRPG.....WYRSDGMDVWGQGTIVVSS 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	73.0	123	2	S26794 Ig heavy chain V r
2	494.5	71.8	141	2	S31669 Ig heavy chain V r
3	490	71.1	123	2	S31114 Ig heavy chain - h
4	485	70.4	125	2	S30531 Ig heavy chain V r
5	481	69.8	140	2	S31588 Ig heavy chain V r
6	479	69.5	143	2	S23624 Ig heavy chain V r
7	477.5	69.3	122	2	E36005 Ig heavy chain V r
8	475	68.9	119	2	C36005 Ig heavy chain V r
9	473	68.7	117	2	S34012 Ig heavy chain V r
10	473	68.7	160	2	S05271 Ig heavy chain pre
11	470.5	68.3	118	2	S31105 Ig heavy chain (su
12	470.5	68.3	128	2	S26790 Ig heavy chain V r
13	469.5	68.1	147	2	I37780 Ig variable region
14	469	68.1	119	2	S31108 Ig heavy chain - h
15	468.5	68.0	128	2	S48797 Ig heavy chain V r
16	468	67.9	120	2	F36005 Ig heavy chain V r
17	467.5	67.9	119	2	S48798 Ig heavy chain V r
18	467	67.8	119	2	S31107 Ig heavy chain - h
19	466	67.6	117	2	S78486 Ig heavy chain V r
20	465.5	67.6	128	2	S26786 Ig heavy chain V r
21	465	67.5	123	2	S30532 Ig heavy chain V r
22	464.5	67.4	114	2	S31120 Ig heavy chain - h
23	463.5	67.3	120	2	E49590 Ig heavy chain V r
24	463	67.2	98	2	S26940 Ig heavy chain V r
25	461	66.9	119	2	D36005 Ig heavy chain V r
26	461	66.9	152	2	B26471 Ig heavy chain pre
27	459	66.6	127	2	S19878 Ig heavy chain V r
28	458.5	66.5	128	2	S31595 Ig heavy chain V r
29	458	66.5	116	2	S21979 Ig heavy chain V-g

30	457.5	66.4	136	2	S31587 Ig heavy chain V r
31	456.5	66.3	124	2	S20782 Ig heavy chain V r
32	456	66.2	121	2	I55673 Ig heavy chain - h
33	454	65.9	134	2	S31679 Ig heavy chain V r
34	453	65.7	138	2	S31666 Ig heavy chain V r
35	453	65.7	140	2	S31686 Ig heavy chain V r
36	452.5	65.7	114	2	S46390 Ig heavy chain V r
37	452	65.6	121	2	S31118 Ig heavy chain - h
38	452	65.6	123	2	S31509 Ig heavy chain - h
39	451.5	65.5	110	2	PH1652 Ig heavy chain V r
40	451.5	65.5	116	2	S17080 Ig heavy chain V-g
41	451.5	65.5	118	2	S31116 Ig heavy chain - h
42	451	65.5	134	2	S31699 Ig heavy chain V r
43	450	65.3	121	2	G36005 Ig heavy chain V r
44	449.5	65.2	140	2	S70442 Ig heavy chain pre
45	449	65.2	130	2	I37783 Ig variable region

ALIGNMENTS

```

RESULT 1
S26794
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S26794
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene f
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MOR>
A:Cross-references: EMBL:X61011
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match          73.0%; Score 503; DB 2; Length 123;
Best Local Similarity 77.4%; Pred. No. 4.8e-38;
Matches 103; Conservative 8; Mismatches 10; Indels 12; Gaps 3;

QY 1 EVQLLESGVSGGGLVPRPGSLRLSCAASGFTFSSYSMMHWVQGPCKGLEWYSTISNSMT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db. 1.EVOL---VESGGGLVQPGSLRLSCAASGFTFSSYSMMHWVQAPCKGLEWYSISSSS 56
QY 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAETAVYVCARDSR--SNFLRWVRSQGM 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYCAISKYDENY-----GM 110
QY 119 DWVGQGTIVVSS 131
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 DWVGQGTIVVSS 123

RESULT 2
S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669
R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CU1>
A:Cross-references: EMBL:214212; NID:g30959; PIDN:CAA78581.1; PID:g30960
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

```


Query Match	69.5%;	Score 479;	DB 2;	Length 143;
Best Local Similarity	76.3%;	Pred. No. 7.8e-36;		
Matches 100; Conservative	7;	Mismatches 10;	Indels 14;	Gaps 3;

[illegible]

RESULT 7
E36005

Ig heavy chain V region (M72) - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1990 #sequence_rev:150 21-Dec-1990 #text_change 16-Dec-1998
 C:Accession: E36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:2117273
 A:Accession: E36005
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <SCH>
 A:Cross-references: GB:M34030
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDX1
 A:Cross-references: GDB:118731; OMTM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 C:15-98/Domain: immunoglobulin homology <IMM>

Query Match	69.3%	Score 477.5	DB 2:	Length 122;
Best Local Similarity	74.0%	Pred. No. 9e-36;		
Matches 97; Conservative	10;	Mismatches	15;	Indels 9; Gaps 3;

[illegible]

RESULT 8

C36005
Ig heavy chain V region (30p1) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
P:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilisation of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: C36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

	Query Match	68.9%;	Score 475;	DB 2;	Length 119;
	Best Local Similarity	72.5%;	Pred. No. 1.5e-35;		
	Matches	95;	Conservative	10;	Mismatches 14; Indels 12; Gaps 2
Oy	1	EVOLLSESVEGAGGGLVPRPGSLRLSCAASGFFPSSYSMHVWROQPGKGLIEWSSISNSMT	60		
Db	1	EVOLL-----ESGGGLVPRPGSLRLSCAASGFFPSSYSMHVWROQPGKGLIEWSSISNSG	56		
Oy	61	YIYVADAVKGRFTISRDNKNSLYLQNMSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV	120		
Db	57	STYVADSVKGRFTISRDNKNSMTLYLQNMSLRAEDTAVYYCARDAGMGS-----GFDFY	108		
Oy	121	WGQGTIVTVYSS	131		
Db	109	WGQGTIVTVYSS	119		

RESULT 9
S34012
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S34012, S30358
R:Mariette, X.; Tsapis, A.; Brouet, J.C.

RESULT 9

Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence.revision 10-Nov-1995 #text-change 16-Aug-1996
C:Accession: S34012; S30538
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34012
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <MAR>
A:Cross-references: EMBL:Z18324
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:;15-95/Domain: immunoglobulin homology <IM>

Query Match	68.7%	Score 473;	DB 2;	Length 117;
Best Local Similarity	74.8%	Pred. No. 2.2e-35;		
Matches 98;	Conservative 7;	Mismatches 12;	Indels 14;	Gaps 3;

[illegible]

RESULT 10

Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #extl_change 16-Aug-1996
C:Accession: S05271; 504602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <K151>
A:Cross-references: EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains

A:Reference number: S04601; MUID:89296497; PMID:2500644

A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <RIS2>
A:Cross-references: EMBL:X14584
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence; status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment); status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.7% Score 473; DB 2; Length 160;
Best Local Similarity 73.9% Pred. No. 3e-35;
Matches 99; Conservative 9; Mismatches 14; Indels 12; Gaps 3;

QY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 60
DB 20 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 60
QY 61 YIYVADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDG 117
DB 76 YIYVADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDG 130
QY 118 MDVWGQGTIVYSS 131
DB 131 MDVWGQGTIVYSS 144

RESULT 11

19 heavy chain (subclass IgM) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
A:Accession: S31105
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31105
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RAA>
A:Cross-references: EMBL:X63081; NID:932648; PIDN:CAA44803.1; PID:932649
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.3% Score 470.5; DB 2; Length 118;
Best Local Similarity 72.5% Pred. No. 3.6e-35;
Matches 95; Conservative 7; Mismatches 16; Indels 13; Gaps 2;
QY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 60
DB 1 QVOL-----VESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 56
QY 61 YIYVADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDGMDV 120
DB 57 YIYVADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDGMDV 107
QY 121 WGQGTIVYSS 131
DB 108 WGQGTIVYSS 118

RESULT 12

S26790
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
A:Accession: S26790
R:Raaphorst, F.M.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene f

A:Reference number: S26786; MUID:92111632; PMID:1770251
A:Accession: S26790
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <MON>
A:Cross-references: EMBL:X61013; NID:932798; PIDN:CAA4347.1; PID:91335128
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.3% Score 470.5; DB 2; Length 128;
Best Local Similarity 73.5% Pred. No. 4e-35;
Matches 97; Conservative 7; Mismatches 23; Indels 5; Gaps 2;

QY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 60
DB 1 QVOL-----VESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 56
QY 61 YIYVADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDG 119
DB 57 YIYVADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDG 116
QY 120 VMGQGTIVYSS 131
DB 117 VMGQGTIVYSS 128

RESULT 13

19 variable region (VDJ) (clone T20-11) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
A:Accession: I37780; S25474
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed b
A:Reference number: A36876; MUID:94119917; PMID:8290556
A:Accession: I37780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <RES>
A:Cross-references: EMBL:X67943; NID:933578; PIDN:CAA48130.1; PID:933579
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 68.1% Score 469.5; DB 2; Length 147;
Best Local Similarity 72.5% Pred. No. 5.7e-35;
Matches 95; Conservative 9; Mismatches 20; Indels 7; Gaps 2;
QY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 60
DB 14 EVOL-----VESGGGLVYKPGGSLRLSCAASGFTFSYSSMHVVRGPGKGLEWVSSISNSNT 69
QY 61 YIYVADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDGMDV 120
DB 70 EKYVADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYVCARDSRYSNFLRWVRSDGMDV 126
QY 121 WGQGTIVYSS 131
DB 127 WGQGTIVYSS 137

RESULT 14

S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
A:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31108
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:1-98/Domain: immunoglobulin homology <IIma>

Query Match	68.1%;	Score 469;	DB 2;	Length 119;
Best Local Similarity	72.5%;	Pred. No. 5e-35;		
Matches 95; Conservative	8;	Mismatches 16;	Indels 12;	Gaps 2

QY	1	EVOLLSSGVSGGGGLVKKPGGSLRLSCAASGFFESSYSHMWROCPGKGLEWVSAISNSNT	60
Db	1	EVOLL-----ESGGGLVQPGGSLRLSCAASGFFESSYASMSVWROAPGKGLEWVSAISGSGG	56
QY	61	YIYDAVAVGREFITSDNAKNSLYLOMASLRLREHFAVYVCARDGSRYSFLRLMWASDCMDV	120
Db	57	STIYDAVSAGREFITSDNKNKNTLYLOMNSLRLREDAVYVCAKDKRLRG-----TFDY	108
QY	121	WGCGTIVAVSS	131
Db	109	WGCGTILVAVSS	119

RESULT 15

Ig heavy chain V region (anti-Sm, VH3/DXP4/5H6) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
 C:Accession: S48797, S26893
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 Submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S48797
 A:Molecule type: mRNA
 A:Residues: 1-128 <MAH>
 A:Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAH86512.1; PID:g1340168
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Dlewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PIDN:1404388
 A:Accession: S26893
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAH78220.1; PID:g32923
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 C:15-98/Domain: Immunoglobulin homology <IMH>

Query Match	68.0%	Score 468.5;	DB 2,	Length 128;
Best Local Similarity	71.6%;	Pred. No. 6e-35;		
Matches 96; Conservative	11;	Mismatches	9;	Gaps 3

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 04:44:09 ; Search time 33 Seconds
(without alignments)
186.682 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGLVLRPG.....WVRSDGMDVWGQTTIVSS 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432.5	62.8	136	1	HY16_MOUSE
2	429.5	62.3	122	1	HY3G_HUMAN
3	424.5	61.6	114	1	HY3B_HUMAN
4	419	60.8	117	1	HY3C_HUMAN
5	407.5	59.1	122	1	HY3H_HUMAN
6	406.5	59.0	122	1	HY3A_HUMAN
7	404	58.6	121	1	HY3J_HUMAN
8	402	58.3	120	1	HY3E_HUMAN
9	400	58.1	115	1	HY3F_HUMAN
10	397.5	57.7	116	1	HY3T_HUMAN
11	395	57.3	98	1	HY57_MOUSE
12	391.5	56.8	119	1	HY38_MOUSE
13	391	56.7	119	1	HY3I_HUMAN
14	390	56.6	117	1	HY01_CANFA
15	389.5	56.5	114	1	HY01_CANFA
16	389.5	56.5	120	1	HY3U_HUMAN
17	388.5	56.3	123	1	HY22_MOUSE
18	388	56.3	123	1	HY24_MOUSE
19	386.5	56.1	116	1	HY05_CARAU
20	386	56.0	115	1	HY3D_HUMAN
21	384	55.7	123	1	HY23_MOUSE
22	383	55.6	123	1	HY18_MOUSE
23	383	55.6	123	1	HY25_MOUSE
24	381	55.3	116	1	HY3R_HUMAN
25	380.5	55.2	111	1	HY35_MOUSE
26	380	55.2	117	1	HY54_MOUSE
27	380	55.2	117	1	HY59_MOUSE
28	380	55.2	123	1	HY19_MOUSE
29	378	54.8	144	1	HY26_MOUSE
30	377.5	54.8	97	1	HY56_MOUSE
31	377	54.7	117	1	HY51_MOUSE
32	376.5	54.6	122	1	HY21_MOUSE
33					

34	375	54.4	115	1	HY32_MOUSE	P01801 mus musculu
35	373	54.1	113	1	HY30_MOUSE	P01799 mus musculu
36	373	54.1	117	1	HY58_MOUSE	P18529 mus musculu
37	372.5	54.1	122	1	HY20_MOUSE	P01789 mus musculu
38	371.5	53.9	117	1	HY3Q_HUMAN	P01776 homo sapien
39	371.5	53.9	119	1	HY3M_HUMAN	P01774 homo sapien
40	370.5	53.8	119	1	HY3N_HUMAN	P01811 mus musculu
41	370	53.7	117	1	HY41_MOUSE	P01817 mus musculu
42	369.5	53.6	119	1	HY37_MOUSE	P01810 mus musculu
43	367.5	53.3	119	1	HY40_MOUSE	P01809 mus musculu
44	367	53.3	118	1	HY39_MOUSE	P01796 mus musculu
45	366	53.1	113	1	HY27_MOUSE	

ALIGNMENTS

RESULT 1
ID HY16_MOUSE STANDARD: PRT; 136 AA.
AC P01783:
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajesky K.,
RA Baltimore D.,
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adelungo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).

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EMBL: J00522; A015290.1; -
PIR: E90809; G1MS21.
PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1
FT SIGNAL <1 136
FT CHAIN 17 136
FT DOMAIN 115 119
FT DOMAIN 120 136
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 115
FT CONFLICT 120 120
FT NON_TER 136 136
HYAD -> DYAH (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 62.8%; Score 432.5; DB 1; Length 136;
Best Local Similarity 64.9%; Pred. No. 4.2e-36;
Matches 85; Conservative 16; Mismatches 19; Indels 11; Gaps 2;

QY 1 EVOLLESGVSGGLVKGPGSLRLSCASGFTFSYSMHVNRGPGKGLWVSSISNSNT 60
DB 17 DVQL---VESGGGLVQPGGSKRLSCASGFTFSFSGMHVNRQAEKGLWVAITSGSS 72
QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYCCARDSRYSNPLRWVSDGMDV 120
DB 73 TLHADTVKGRFTISRDNKNSLYLQMSLRAEHTAVYCCARDSRYSNPLRWVSDGMDV 125
QY 121 WGQGTIVYSS 131
DB 126 WGQGTIVYSS 136

RESULT 2

HY3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02051; M3HUM.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 122 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 62.3%; Score 429.5; DB 1; Length 122;
Best Local Similarity 67.7%; Pred. No. 7.3e-36;
Matches 84; Conservative 14; Mismatches 19; Indels 7; Gaps 2;

QY 9 VESGGGLVKGPGSLRLSCASGFTFSYSMHVNRGPGKGLWVSSISNSNTYIYADAV 68
DB 5 VESGGGLVKGPGSLRLSCASGFTFSYSMHVNRGPGKGLWVAVISYGBBKRYABSV 64
QY 69 KGRFTISRDNKNSLYLQMSLRAEHTAVYCCARD-SRYSNPLRWVSDGMDVWGQGTIV 127
DB 65 KGRFTISRDNKNSLYLQMSLRAEHTAVYCCARDRPLTGBY-----RAFNWYGQGTIV 118
QY 128 IVSS 131
DB 119 IVSS 122

RESULT 3
HY3B_HUMAN STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=63273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC MADDENSTROM'S MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02046; M3HOM.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IGV_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 114 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FBA18A07B CRC64;

Query Match 61.6%; Score 424.5; DB 1; Length 114;
Best Local Similarity 65.6%; Pred. No. 2.1e-35;
Matches 86; Conservative 15; Mismatches 13; Indels 17; Gaps 3;

QY 1 EVOLLESGVSGGLVKGPGSLRLSCASGFTFSYSMHVNRGPGKGLWVSSISNSNT 60
DB 1 QVQL---VDSGGGLVQPGGSKRLSCASGFTFSNDMNWVROAPGKGLWLSFTIGSGS 56
QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYCCARDSRYSNPLRWVSDGMDV 120
DB 57 TIYADVSKGRFTISRDNKNSLYLQMSLRAEHTAVYCCARG-----WLLN----- 103
QY 121 WGQGTIVYSS 131
DB 104 WGQGTIVYSS 114

RESULT 4

HY3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]

FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT STRAND 14 15
 FT STRAND 18 25
 FT HELIX 29 31
 FT STRAND 34 39
 FT STRAND 41 42
 FT STRAND 45 51
 FT STRAND 53 54
 FT STRAND 58 60
 FT STRAND 62 64
 FT HELIX 65 65
 FT STRAND 66 67
 FT TURN 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 116
 FT STRAND 120 124
 FT NON_TER 125 126
 SO SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 59.1%; Score 407.5; DB 1; Length 126;
 Best Local Similarity 62.6%; Pred. No. 1.2e-33;
 Matches 82; Conservative 18; Mismatches 26; Indels 5; Gaps 2;

QY 1 EVOLLESGVGGGLVPGGSLRLSCAASGFTSSYSMMHWQPGKGLRWVSSISNSMT 60
 DB 1 QVOL---VESGGGVYQGRSLRLSCSSSGFTSSYSMMHWQAPGKGLRWVAILIMDDGS 56
 QY 61 YIYVADAVKGRFTISRDNKSLYLQNSLRAEHTAVYYCA--RDSRYSNFLRWVRSQGM 120
 DB 57 DQHYADSVKGRFTISRDNKSLYLQNSLRAEHTAVYYCA--RDSRYSNFLRWVRSQGM 115
 QY 121 WGGGTIVYSS 131
 DB 116 WGGGTIVYSS 126

RESULT 7
 HV3J_HUMAN STANDARD; PRT; 122 AA.
 ID P01771;
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 19 heavy chain V-III region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN TRO).
 RX MEDLINE=76023781; PubMed=809331;
 RA Kitzin H., Altevogt P., Ruban E., Kortt A., Starescik K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA.Tro.),
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup, III;
 RT structure of the complete IgA-molecule."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02045; A1HUTR.
 DR HSSP: P01772; 2F84.
 GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-LIKE.
 DR InterPro: IPR003006; IG-MHC.
 DR InterPro: IPR003596; IG-V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv_1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 108
 FT MOD_RES 1 1
 FT NON_TER 122 122
 SO SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 59.0%; Score 406.5; DB 1; Length 122;
 Best Local Similarity 58.6%; Pred. No. 1.4e-33;
 Matches 78; Conservative 19; Mismatches 23; Indels 13; Gaps 3;

QY 1 EVOLLESGVGGGLVPGGSLRLSCAASGFTSSYSMMHWQPGKGLRWVSSISNSMT 60
 DB 1 QVOL---VESGGGVYQGRSLRLSCSSSGFTSSYSMMHWQAPGKGLRWVAILIMDDGS 56
 QY 61 YIYVADAVKGRFTISRDNKSLYLQNSLRAEHTAVYYCA--RDSRYSNFLRWVRSQGM 118
 DB 57 TLVYADSVKGRFTISRDNKSLYLQNSLRAEHTAVYYCA--RDSRYSNFLRWVRSQGM 109
 QY 119 DWGGGTIVYSS 131
 DB 110 BYWGGGTIVYSS 122

RESULT 8
 HV3J_HUMAN STANDARD; PRT; 121 AA.
 ID P01771;
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 19 heavy chain V-III region HLT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 RT cryoimmunoglobulin IgG H1L."
 RL Biochemistry 18:553-560(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02054; G1HRLH.
 DR HSSP: P01772; 2F84.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-LIKE.
 DR InterPro: IPR003006; IG-MHC.
 DR InterPro: IPR003596; IG-V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv_1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT NON_TER 121 121
 SO SEQUENCE 121 AA; 13566 MW; 480FC3610EF5DAB CRC64;

Query Match 58.6%; Score 404; DB 1; Length 121;
 Best Local Similarity 62.6%; Pred. No. 2.5e-33;
 Matches 77; Conservative 15; Mismatches 25; Indels 6; Gaps 1;

QY 9 VESGGGLVKGPGSLRLSCAASGFTFSYSMHWVRGPGKGLVWSSISNSNTIYYADAV 68
 DB 5 VOAGGGVQPGKSLRLSCAASGFTFSYSGMHVVRAPKGLVWAVINYSRITYGDSV 64
 QY 69 KGRFTISDNKNSLYLQMSLRAEHVAVYVCARDRSYNFLRWSDGMDVGGCTTVI 128
 DB 65 KGRFTISDNKNSLYLQMSLRAEHVAVYVCARDRSYNFLRWSDGMDVGGCTTVI 118
 QY 129 VSS 131
 DB 119 VSS 121

RESULT 9

HV3E_HUMAN STANDARD: PRT; 120 AA.
 ID HV3E_HUMAN
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region BRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71117674; PubMed=65324;
 RA Capra J.D., Hopper J.E.;
 RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
 RT individual patient. III. The complete amino acid sequence of the VH
 RT region of the IgM paraprotein."
 RL Immunohematology 13:995-999(1976).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
 CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
 CC TYPE.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02049; M3HUBW.
 DR HSSP: P01772; 2PBA.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig-MHC.
 DR InterPro: IPR003596; Ig-V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 111
 FT NON_TER 120 120 IG-LIKE.
 SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match 58.3%; Score 402; DB 1; Length 120;
 Best Local Similarity 68.8%; Pred. No. 3.8e-33;
 Matches 86; Conservative 11; Mismatches 22; Indels 6; Gaps 3;

QY 1 EVLLSGVESGGGLVKGPGSLRLSCAASGFTFSYSMHWVRGPGKGLVWSSISNSNT 60
 DB 1 EVLLSGVESGGGLVKGPGSLRLSCAASGFTFSYSGMHVVRAPKGLVWAVINYSRITYGDSV 56
 QY 61 YIYADAVKGRFTISDNKNSLYLQMSLRAEHVAVYVCARDRSYNFLRWSDGMDV 120
 DB 57 Q-YIYADSVKGRFTISDNKNSLYLQMSLRAEHVAVYVCARDRSYNFLRWSDGMDV 114
 QY 121 WGGGT 125
 DB 115 WGGGT 119

RESULT 10
 HV3F_HUMAN

ID HV3F_HUMAN STANDARD: PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region BRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT IgA2 immunoglobulin of the A2m (2) allotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02050; A2HUBW.
 DR HSSP: P01789; 1MCP.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig-MHC.
 DR InterPro: IPR003596; Ig-V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 111
 FT NON_TER 115 115 IG-LIKE.
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7D52DCF4 CRC64;

Query Match 58.1%; Score 400; DB 1; Length 115;
 Best Local Similarity 61.8%; Pred. No. 5.8e-33;
 Matches 81; Conservative 18; Mismatches 16; Indels 16; Gaps 3;

QY 1 EVLLSGVESGGGLVKGPGSLRLSCAASGFTFSYSMHWVRGPGKGLVWSSISNSNT 60
 DB 1 EVLLSGVESGGGLVKGPGSLRLSCAASGFTFSYSGMHVVRAPKGLVWAVINYSRITYGDSV 56
 QY 61 YIYADAVKGRFTISDNKNSLYLQMSLRAEHVAVYVCARDRSYNFLRWSDGMDV 120
 DB 57 -TYIADSVKGRFTISDNKNSLYLQMSLRAEHVAVYVCARDLAAR-----L 104
 QY 121 WGGGTIVSS 131
 DB 105 FGKGTIVSS 115

RESULT 11

HV3T_HUMAN STANDARD: PRT; 116 AA.
 ID HV3T_HUMAN
 AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Berrman J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IgM-molecule."
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).

```

RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.:
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02064; M3HGL.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR SMART: SM00406; IGV: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match
Best Local Similarity 57.7%; Score 397.5; DB 1; Length 116;
Matches 84; Conservative 7; Mismatches 25; Indels 15; Gaps 3;

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSSISNSNT 60
DB 1 EVQLL...VESGGDLVQPGKSLRLSCAASGFTFBBLGNTWYKQAPKGLWVAVNIKZBGS 56
OY 61 YIYVADAVKGRFTISRDNANKNSLYLQNSLRARHTAVYVCARSDSYNFLRWVSDGMV 120
DB 57 ZBYVDVSKGRFTISRDNANKNSLYLQNSLVEDTALTYCARG-----W----GGSDY 105
OY 121 WCGGTVTVSS 131
DB 106 WCGGTVTVST 116

RESULT 12
HV37_MOUSE STANDARD; PRT; 98 AA.
ID HV37_MOUSE
AC P18528;
DR 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DR 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RA "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: J05051; HVMS96.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR Pfam: PF00047; IGV: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 10730 MW; 1C67CA9AAAAA1282 CRC64;
```

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SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match
Best Local Similarity 57.3%; Score 395; DB 1; Length 98;
Matches 76; Conservative 12; Mismatches 10; Indels 4; Gaps 1;

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSSISNSNT 60
DB 1 EVQLL...VESGGDLVQPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVAVNIKZBGS 56
OY 61 YIYVADAVKGRFTISRDNANKNSLYLQNSLRARHTAVYVCARSDSYNFLRWVSDGMV 120
DB 57 ZBYVDVSKGRFTISRDNANKNSLYLQNSLVEDTALTYCARG-----W----GGSDY 105

RESULT 13
HV38_MOUSE STANDARD; PRT; 119 AA.
ID HV38_MOUSE
AC P01808;
DR 21-JUN-1986 (Rel. 01, Created)
DR 21-JUN-1986 (Rel. 01, Last sequence update)
DR 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 1601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE
RC MEDLINE=7923895; PubMed=111245;
RA Reid D.N., Rudikoff S., Krutzsch H., Potter M.;
RA "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-Jackson myeloma proteins and
RT its potential role in generating diversity in
RT complementarity determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC -1- THAT BINDS GALACTAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02078; AVMS16.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR Pfam: PF00047; IGV: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match
Best Local Similarity 56.8%; Score 391.5; DB 1; Length 119;
Matches 79; Conservative 15; Mismatches 24; Indels 13; Gaps 2;

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSSISNSNT 60
DB 1 EVQLL...VESGGDLVQPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVAVNIKZBGS 56
OY 61 YIYVADAVKGRFTISRDNANKNSLYLQNSLRARHTAVYVCARSDSYNFLRWVSDGMV 120
DB 57 TINTPTSLKDKFTISRDNANKNSLYLQNSKVRSDTALTYCARLGYGYF-----DV 107

RESULT 14
HV31_HUMAN STANDARD; PRT; 119 AA.
ID HV31_HUMAN
AC P01770;
```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN NCBI
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponslingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN MYELOMA
CC PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A91668; GIHUNI.
DR HSSP; P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyritolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA: 13242 MW: C96935A6E55E165B CRC64;
Query Match 56.7%; Score 391; DB 1; Length 119;
Best Local Similarity 60.9%; Pred. No. 4.7e-32;
Matches 81; Conservative 15; Mismatches 21; Indels 16; Gaps 3;
QY 1 EVOLLESGVSGGLVPRGSGSLRLSCAASGFTFSYSNMHWYRQPGKGLVWVSSISNSNT 60
DB 1 QVQL-----VQSGGVVQPGRLRLSCAASGFTFSRYTHWRAQAPGKLEWVAVMSYGB 56
QY YYYADAVKGRFTISRDNKASLTLYQMNSLAEHTAVYVCARDSDRYSLFLWVRSDGMDV 120
DB 57 BKHTADSYNGRFTISRDNKNTLYLNMNSLRPEDTAVYTCAR-----INDTAIEF 106
QY 121 --WGQGTIVIVSS 131
DB 107 AHMGQGLTVIVSS 119
RESULT 15
ID HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN NCBI
RP SEQUENCE OF 1-112.
RX MEDLINE=77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RT immunoglobulin heavy chains."
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP SEQUENCE OF 113-117.
RX MEDLINE=80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain."
RL Mol. Immunol. 16:565-570(1979).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90403; MHDGMO.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12703 MW: FCE07309E0A84B35 CRC64;
Query Match 56.6%; Score 390; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 5.8e-32;
Matches 85; Conservative 9; Mismatches 18; Indels 24; Gaps 4;
QY 1 EVOLLESGVSGGLVPRGSGSLRLSCAASGFTFSYSNMHWYRQPGKGLVWVSSISNSNT 60
DB 1 EVKL-----VESGGLVPRGSGSLRLSCVAGFTFSNGMSWVRQDPGEGLOVWVADISSG 55
QY YYYADAVKGRFTISRDNKASLTLYQMNSLAEHTAVYVCARDSDRYSLFLWVRSDGMDV 115
DB 56 QYYADAVKGRFTISRDNKNTLYLQMDLRVEDTAVYVCATGDIETPRY----- 106
QY 116 DGMVWGQGTIVIVSS 131
DB 107 -----FGQGTIVIVSS 117

Search completed: September 24, 2003, 06:27:32
Job time : 34 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 05:40:25 ; Search time 75 Seconds
(without alignments)
450.732 Million cell updates/sec

Title: US-09-848-798A-28

Perfect score: 689

Sequence: 1 EVOLLESGVESGGGLVPRGK.....WVRSDGMDVMGQTTVIYSS 131

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500.5	72.6	471	4	08TC77
2	477.5	69.3	118	4	09UL91
3	466.5	67.7	494	4	096K68
4	463	67.2	597	4	096BB9
5	461.5	67.0	573	4	08WU38
6	455.5	66.1	613	4	08WU38
7	453.5	65.7	473	11	091Z05
8	453	65.7	113	4	09UL90
9	450	65.3	121	4	09UL71
10	445.5	64.7	487	11	099KA4
11	432	62.7	116	4	09UL93
12	430	62.4	499	4	08N5K4
13	427.5	62.0	112	4	09HCC1
14	426.5	61.9	122	4	09UL84
15	426	61.8	119	11	0920E7
16	423.5	61.5	118	4	09UL72

17	423.5	61.5	147	4	09Y509	Q9Y509	homo sapien
18	413	59.9	493	4	08NCL6	08NCL6	homo sapien
19	401	58.2	479	11	091MP5	091MP5	mus musculus
20	395	57.3	95	4	09ULB6	09ULB6	homo sapien
21	384	55.7	480	11	091XE1	091XE1	homo sapien
22	381.5	55.4	469	11	08R3V9	08R3V9	mus musculus
23	376	54.6	486	11	091Z07	091Z07	mus musculus
24	373.5	54.2	298	11	09QYR0	09QYR0	mus musculus
25	369.5	53.6	484	11	08VEA0	08VEA0	mus musculus
26	368	53.4	131	4	09UL88	09UL88	homo sapien
27	365.5	53.0	437	11	09R1A4	09R1A4	homo sapien
28	362	52.5	104	4	09UL87	09UL87	homo sapien
29	357	51.8	521	4	08N4Y9	08N4Y9	homo sapien
30	349.5	50.7	124	6	09N0M4	09N0M4	oryzolaus
31	347	50.4	112	4	09UGP3	09UGP3	homo sapien
32	346.5	50.3	124	6	09N0W6	09N0W6	oryzolaus
33	336.5	48.8	124	4	09UL92	09UL92	homo sapien
34	325	47.2	125	4	09UL95	09UL95	homo sapien
35	320.5	46.5	159	4	096Q50	096Q50	homo sapien
36	319	46.3	142	11	0924Q1	0924Q1	mus musculus
37	317	46.0	117	11	09QXR9	09QXR9	mus musculus
38	315.5	45.8	109	11	09UL75	09UL75	mus musculus
39	315.5	45.8	482	11	08K172	08K172	mus musculus
40	314.5	45.6	143	11	091VA2	091VA2	mus musculus
41	314.5	45.6	143	11	0924R7	0924R7	mus musculus
42	313	45.4	484	11	099LA6	099LA6	mus musculus
43	311.5	45.2	143	11	0924R0	0924R0	mus musculus
44	311	45.1	117	11	09QXR0	09QXR0	mus musculus
45	311	45.1	142	11	0924Q2	0924Q2	mus musculus

ALIGNMENTS

RESULT 1

08TC77 PRELIMINARY: PRT: 471 AA.

AC 08TC77:

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Spleen;

RA Strausberg R.;

RU	Submitted (Feb-2002) to the EMBL/Genbank/DBJ databases.
DR	EMBL: BC024288; AAH24288.1; -
DR	InterPro: IPR007110; IG_Like.
DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003596; IG_V.
DR	Pfam: PF00047; Ig_4.
DR	SMART: SM00406; IGV_1.
DR	PROSITE: PS50835; IG_Like; 4.
DR	PROSITE: PS00290; IG_MHC; 2.
KW	Hypothetical protein.
SQ	SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match

Best Local Similarity 72.6%; Score 500.5; DB 4; Length 471;

Matches 102; Conservative 8; Mismatches 12; Indels 9; Gaps 3;

OY	1	EVOLLESGVESGGGLVPRGSLRLSCAASGTFSSSWHWYRGQKGLLEWSSISNNT	60
DB	20	EVOL-----VESGGGLVPRGSGSLRLSCAASGTFSSSWHWYRGQKGLLEWSSISNNT	75
OY	61	YIYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYVCARDISYNFLRWVRSDGMDV	120
DB	76	YIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYVCARDISYNFLRWVRSDGMDV	130

OY 121 MGCGTIVTSS 131
 Db 131 MGCGTIVTSS 141

RESULT 2

O9UL91 PRELIMINARY; PRT; 118 AA.
 AC O9UL91
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Mucin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Mucin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035023; AAD56259.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT 118
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 69.3%; Score 477.5; DB 4; Length 118;
 Best Local Similarity 75.6%; Pred. No. 1.3e-39;
 Matches 99; Conservative 7; Mismatches 10; Indels 15; Gaps 3;

OY 1 EVOLLSGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWSSISNSNT 60
 Db 1 EVOL---VESGGGLVQPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWSSISNT 56
 OY 61 YIYADAVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCAR-DSRYSNFLRWVRSDGMD 119
 Db 57 TIYADSVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCARDS-----SEAFD 106
 OY 120 VMCGGTIVTSS 130
 Db 107 VMCGGTIVTSS 117

RESULT 3

O96K68 PRELIMINARY; PRT; 494 AA.
 AC O96K68
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Hypothetical protein FLJ14473.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosofri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
 RA Niinomiya K., Iwayanagi T.,
 RT "NPD human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB55072.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE64C0E CRC64;

Query Match 67.7%; Score 466.5; DB 4; Length 494;
 Best Local Similarity 72.5%; Pred. No. 1.3e-37;
 Matches 95; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

OY 1 EVOLLSGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWSSISNSNT 60
 Db 20 EVOL---VESGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPGKLEWSSISNSRD 75
 OY 61 YIYADAVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCARDSRYSNFLRWVRSDGMD 120
 Db 76 YIYRDSVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCARDS-----CNGAICVGFSP 130
 OY 121 MGCGTIVTSS 131
 Db 131 MGCGTIVTSS 141

RESULT 4

O96BB9 PRELIMINARY; PRT; 597 AA.
 AC O96BB9
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8BECE263D9 CRC64;

Query Match 67.2%; Score 463; DB 4; Length 597;
 Best Local Similarity 72.0%; Pred. No. 3.7e-37;
 Matches 95; Conservative 12; Mismatches 17; Indels 8; Gaps 3;

OY 1 EVOLLSGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWSSISNSNT 60
 Db 20 EVOL---ESGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPGKLEWSSAISGSG 75
 OY 61 YIYADAVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCARDSR-YSNFLRWVRSDGMD 119
 Db 119 YIYADAVKGRFTISRDNAKNSLYLQMSLRRAEDTAIVYCARDSR-YSNFLRWVRSDGMD 119

Db	Qy	Db
76	SIYYADSVKGRRTISRDNSTPDTLYLQMNSLAEEDTAVYYCAKDKPRGISASGNITRE---	D 132
120	VMGQGITVTVSS	131
133	YMGQGITVTVSS	144

RESULT 5	PRELIMINARY;	PRT;	573 AA.
08MWJ38			
ID	Q8MWJ38		
AC	Q8MWJ38;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TrISSE-Trans11;		
RA	Straussberg R.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC021276; AAH21276.1; -		
DR	InterPro: IPR007110; Ig_Like.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Plan; PF00047; Ig_4.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		
DR	PROSITE; PS00290; IG_MHC; 2.		
Q	Hypothetical Protein.		
Q	SEQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;		

Query March	67.0%	Score 461.5;	DB 4,	Length 573;
Best Local Similarity	73.3%	Pred. No. 4.9e-37;		
Matches 96; Conservative	8;	Mismatches 20;	Indels 7;	Gaps 2

QY	1 EVOLLEESGVEGCGGLVPRPGSLRLSCAASGTFPFSSSMHWNRQSPGGGLEWISSNSIT 60 : 20 EQVL-----VESGGGLVPGFSTRLSCAASGTFPFDYAMHWROAPRGGLEWISGISIWSNG 75
Db	
QY	61 YIYYADAVNGRTTISRDNAAKNSLYIQNNMSLAEHTAYTYCCARDSRYSNFLRWVRSDGMdy 120 : 76 STGIADSVAGRTTISRDNAAKNSLYIQNNMSLAEPTALTYCCAKHSGGSYGIGYYY---GMDY 132D

Qy	121	WGQGTTVIVSS	131
Db	133	WGQGTTVTVSS	143

RESULT

ID	ORGANISM	PRELIMINARY	PRF	613 AA
AC	08MUK1			
AC	08MUK1			
DT	01-MAR-2002 (TREMBlrel. 20			
DT	01-MAR-2002 (TREMBlrel. 20			
DT	01-MAR-2003 (TREMBlrel. 23,			
DE	Homo sapiens (Human).			
DE	Hypotheetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC020240; AA020401;			
DR	InterPro: IPR007110; Iq_1like.			
DR	InterPro: IPR003006; Iq_MHC.			
DR	InterPro: IPR003596; Iq_V.			

DR Pfam: PF00047; Ig, 5.
DR SMART: SM00406; Igy, 1.
DR PROSITE: PS50835; IG_LIKE, 5.
DR PROSITE: PS00290; IG_MHC, 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67236 MW; 60C7F5950671E315 CRC64;

Query Match	66.1%;	Score 455.5;	DB 4;	Length 613;
Best Local Similarity	69.4%;	Pred. No. 2.1e-36;		
Matches 93;	Conservative 12;	Mismatches 12;	Indels 17;	Gaps 4

```

QY      3 EVQLDSGGVEGGGLVAPCGSGLRILSCASGTFESSYSHHWVROQPGKGLVSSINSNT 60
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      20 QVQL-----YESGGVYVQPGSRRLRLSCASGTFESSYGHHWVROAKPGKGLVAVISDGS 75

QY      61 YYYAAYAVGRTSLSDNAKNSLYQMSLAETHAYVYCCARDSRYSNPLRWVRSQDM-- 118
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      76 NKYYASVAGRFLISDMSKNTLYIQMSLRREDYAVYVYICK-----W--SEQVET 125

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QY	119	-DVMGQGTIVSS	131
		:	
Db	126	FDIWGQGTMTVSS	139

RESULT 7
Q91205

ID	091205	PRELIMINARY; PRT; 4/3 AA.
AC	091205;	
DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(01-DEC-2001, Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE	Hypothetical 51.9 kDa protein.	
UN	A0044919.	

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases

DR EMBL; BC010327; AAH10327.1;
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_h

DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.

Query Match	65.88;	Score 453.5;	DB 11;	Length 473;
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Best Local Similarity 68.7%; Pred. No. 2.4e-36;
Matches 90; Conservative 13; Mismatches 15; Indels 13; Gaps 3;

[illegible]

QY	121	WGQGTIVVSS	131
		:	
Db	127	WGQGTITVSS	137

RESULT 8

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09UL90
ID 09UL90 PRELIMINARY; PRT; 113 AA.
AC 09UL90:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.".
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.7%; Score 453; DB 4; Length 113;
Best Local Similarity 69.5%; Pred. No. 4.6e-37;
Matches 91; Conservative 8; Mismatches 14; Indels 18; Gaps 2;

QY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTSSYMHVVRGPGKLEWSSISNSNT 60
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOL---VESGGGVVPGGSLRLSCAASGFTSSYGMHVRQAPGKLEWVAIRIDGS 56
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YIYADAVKGRFTISRDNANKSLYLQNSLRAEHTAVYYCARDSRYSNFLRWVSDGMDV 120
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 NKRIADSVKGRFTISRDNANKSLYLQNSLRAEDTAVYYCAKDLNY----- 102
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 WGQGTIVVSS 131
   ||||| |||||
Db 103 WGQGTIVVSS 113
   ||||| |||||

RESULT 9
09UL71 PRELIMINARY; PRT; 121 AA.
ID 09UL71:
AC 09UL71:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.".
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCEA5D50736 CRC64;

Query Match 65.3%; Score 450; DB 4; Length 121;
Best Local Similarity 68.7%; Pred. No. 9.9e-37;
Matches 90; Conservative 10; Mismatches 21; Indels 10; Gaps 2;

QY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTSSYMHVVRGPGKLEWSSISNSNT 60
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOL---VESGGGVVPGGSLRLSCAASGFTDGYAMHVRQAPGKLEWVSLISDGG 56
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YIYADAVKGRFTISRDNANKSLYLQNSLRAEHTAVYYCARDSRYSNFLRWVSDGMDV 120
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 STYIADSVKGRFTISRDNANKSLYLQNSLRAEDTAVYYCAKGVVTTY-----DREDI 110
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 WGQGTIVVSS 131
   ||||| |||||
Db 111 WGQGTIVVSS 121
   ||||| |||||

RESULT 10
099KA4 PRELIMINARY; PRT; 487 AA.
ID 099KA4:
AC 099KA4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 64.7%; Score 445.5; DB 11; Length 487;
Best Local Similarity 67.2%; Pred. No. 1.5e-35;
Matches 90; Conservative 14; Mismatches 17; Indels 13; Gaps 3;

QY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTSSYMHVVRGPGKLEWSSISNSNT 60
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVOL---VESGGGVVPGGSLRLSCAASGFTSSYAMSVKRTPEKRLRWVATIDGGS 75
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YIYADAVKGRFTISRDNANKSLYLQNSLRAEHTAVYYCARP---SRISNFLRWVSDG 117
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 YTYIPDVKGRFTISRDNANKSLYLQNSHLKSEDTAVYYCARDMGSPYGGYSRFE----- 130
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 MDVWGQGTIVVSS 131
   ||||| |||||
Db 131 -DYWGQGTIVVSS 143
   ||||| |||||

RESULT 11
09UL93

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ID 09UL93      PRELIMINARY;      PRT;      116 AA.
AC 09UL93;
DR 01-MAR-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER      1
FT SEQUENCE      116 AA; 12434 MW; 0DA0348154DD0601 CRC64;

Query Match      62.7%; Score 432; DB 4; Length 116;
Best Local Similarity 67.7%; Pred. No. 5.5e-35;
Matches 88; Conservative 10; Mismatches 18; Indels 14; Gaps 2;

QY 2 VOLLESVESGGGLVPRGGSRLRLSCAASGFTFSYSMMHWYRQPGKLEWVSSISNSNTY 61
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VOL----VESGGGVVPRGGRSLRLSCAASGFTFSYSMMHWYRQPGKLEWVAISYDSN 56
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 IYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARSISNFLRWVSDGDV 121
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 KYVADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCAGGGL-----GLGYW 106
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 GGGTIVYSS 131
   ||| |||||
Db 107 GGGTIVYSS 116
   ||| |||||

RESULT 12
O8N5K4      PRELIMINARY;      PRT;      499 AA.
AC O8N5K4;
DR 01-OCT-2002 (TREMBlrel. 22, Created)
DR 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003597; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00409; IG; 4.

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DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match      62.4%; Score 430; DB 4; Length 499;
Best Local Similarity 66.7%; Pred. No. 5.2e-34;
Matches 92; Conservative 9; Mismatches 19; Indels 18; Gaps 4;

QY 1 EVOLLESVESGGGLVPRGGSRLRLSCAASGFTFSYSMMHWYRQPGKLEWVSSISNSNT 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVOL----VESGGGVVPRGGRSLRLSCATSGFTFDSSGASWYRQAPGKLEWVSSINWNG 75
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 IYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARD--SRYSNFLRWVSDG-- 117
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 STNYADSVKGRFTISRDNKNSLYLQNNSLRVEDTAVYYCARDPTKYC-----SGGSC 128
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 ----MDVWGOGTIVYSS 131
   ||| |||||
Db 129 LGYMDVWKGKTIVYSS 146
   ||| |||||

RESULT 13
O9HCL1      PRELIMINARY;      PRT;      112 AA.
AC O9HCL1;
DR 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a
   human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER      1
FT NON_TER      1
FT SEQUENCE      112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match      62.0%; Score 427.5; DB 4; Length 112;
Best Local Similarity 69.3%; Pred. No. 1.5e-34;
Matches 88; Conservative 8; Mismatches 16; Indels 15; Gaps 3;

QY 1 EVOLLESVESGGGLVPRGGSRLRLSCAASGFTFSYSMMHWYRQPGKLEWVSSISNSNT 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOL----VESGGGVVPRGGRSLRLSCAASGFTFDYGSWYRQAPGKLEWVSGINWNG 56
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 IYYADAVKGRFTISRDNKNSLYLQNNSLRAEHTAVYYCARSISNFLRWVSDGDV 120
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 STGYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCAR--RRYA-----LDY 105
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 WGGGTIV 127
   ||| |||||
Db 106 WGGGTIV 112
   ||| |||||

RESULT 14
O9UL84

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ID 090184      PRELIMINARY;      PRT: 122 AA.
AC 0920E7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; AAD56266.1; -.
DR HSP: P01772; 2PB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SMO0406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT 1
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match      61.8%; Score 426.5; DB 4; Length 122;
Best Local Similarity 66.9%; Pred. No. 2e-34;
Matches 89; Conservative 11; Mismatches 20; Indels 13; Gaps 3;

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```

QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSYSMHWYRQPGKLEWVSISNSNT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 1 EVOL---VESGGGVVOPGSRSLRLSCAASRFTFSNGMHWRQAPGKLEWVAISNDGS 56
QY 61 YIYVADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSRYSNFLRWVSDG--M 118
   :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 57 NKFYADSVKGRFTISRDNKNSLMDLQNSLRAEDTAVYYCAKDER-----GRLVGT 109
QY 119 DWNGGCTLYTVSS 131
   | ||||| | |||
Db 110 DWNGGCTLYTVSS 122

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RESULT 15
ID 0920E7      PRELIMINARY;      PRT: 119 AA.
AC 0920E7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horafitis O., Cotton R.G.H.;
RT "Definition of the idiotope of pterin-mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307937; AAL09421.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SMO0406; IgV_1.

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DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT 1
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match      61.8%; Score 426; DB 11; Length 119;
Best Local Similarity 65.6%; Pred. No. 2.2e-34;
Matches 86; Conservative 12; Mismatches 21; Indels 12; Gaps 2;

QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSYSMHWYRQPGKLEWVSISNSNT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 1 EVOL---VESGGDLVPRGSLRLSCAASGFTSSYMSWVRCPPDKRLEWVAITSSGGS 56
QY 61 YIYVADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSRYSNFLRWVSDGMDV 120
   |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 57 YTYVPSVKGGRFTISRDNKNTLYLQMSLSKSEDTAVYYCARHGDY-----DVGFAY 108
QY 121 WGCGTLYTVSS 131
   ||||| |||||
Db 109 WGCGTLYTVSA 119

```

Search completed: September 24, 2003, 06:29:00
 Job time : 77 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 06:25:35 ; Search time 35 Seconds
(without alignments)
158.363 Million cell updates/sec

Title: US-09-848-798a-28

Perfect score: 689
Sequence: 1 EVOLLESVSGGGGLVKGPG.....WVRSDGMDVWGOGTTIVSS 131Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	100.0	131	3	US-09-240-274-28
2	643	93.3	127	3	US-09-240-274-27
3	507.5	73.7	245	4	US-08-918-148-78
4	488	70.8	249	4	US-10-039-785-53
5	481.5	69.9	109	2	US-08-379-057-32
6	481	69.8	123	2	US-08-665-202-30
7	481	69.8	123	2	US-09-315-574-30
8	479.5	69.6	245	4	US-08-918-148-75
9	478.5	69.4	111	1	US-08-211-202-134
10	473.5	68.7	123	1	US-08-082-623-3
11	470.5	68.3	128	1	US-08-478-039-102
12	470.5	68.3	128	1	US-08-476-349A-102
13	470	68.2	117	4	US-09-025-769B-24
14	470	68.2	123	4	US-09-560-198A-2
15	469.5	68.1	128	1	US-08-478-039-73
16	469.5	68.1	128	1	US-08-476-349A-73
17	467.5	67.9	120	4	US-09-025-769B-38
18	467.5	67.9	120	4	US-09-025-769B-63
19	467.5	67.9	281	4	US-09-025-769B-178
20	463	67.2	117	3	US-08-545-809A-107
21	463	67.2	119	1	US-07-988-925-11
22	463	67.2	119	2	US-08-362-780-11
23	463	67.2	127	3	US-09-240-274-139
24	461.5	67.0	122	5	PCT-US93-08435-12
25	460	66.8	113	3	US-08-974-889-6
26	460	66.8	123	4	US-09-344-587-13
27	458.5	66.5	117	2	US-08-428-197-36

28	458.5	66.5	117	5	PCT-US93-10555-36	Sequence 36, Appl
29	458.5	66.5	122	5	PCT-US93-08435-14	Sequence 14, Appl
30	458.5	66.5	126	3	US-08-983-607-48	Sequence 48, Appl
31	457.5	66.4	126	4	US-09-240-274-152	Sequence 152, App
32	457	66.3	123	4	US-09-560-198A-152	Sequence 4, Appl
33	455.5	66.1	122	5	PCT-US93-08435-43	Sequence 43, Appl
34	454.5	66.0	135	3	US-08-579-378A-20	Sequence 20, Appl
35	454.5	66.0	140	3	US-08-983-607-32	Sequence 32, Appl
36	454.5	66.0	443	5	PCT-US96-13152-4	Sequence 4, Appl
37	453.5	65.8	120	3	US-07-934-373C-4	Sequence 4, Appl
38	453.5	65.8	120	3	US-08-437-642B-4	Sequence 4, Appl
39	453.5	65.8	120	4	US-08-146-206C-4	Sequence 4, Appl
40	453	65.7	112	1	US-08-211-202-133	Sequence 133, App
41	453	65.7	121	2	US-08-887-352B-4	Sequence 4, Appl
42	453	65.7	121	3	US-09-109-207C-4	Sequence 4, Appl
43	453	65.7	121	3	US-09-296-005-4	Sequence 4, Appl
44	453	65.7	125	2	US-08-428-197-1	Sequence 1, Appl
45	453	65.7	125	5	PCT-US93-10555-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-240-274-28
; Sequence 28, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) chain E03
US-09-240-274-28
Query Match
Best Local Similarity 100.0%; Score 689; DB 3; Length 131;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLLESVSGGGGLVKGSGLRSCAAGTFFSSYSHMWROGPKLEWVSSISNSNT 60
DB 1 EVOLLESVSGGGGLVKGSGLRSCAAGTFFSSYSHMWROGPKLEWVSSISNSNT 60
QY 61 YYYADAKGFTTISRDNAKNSLYLQMSLAETHAVYYCARDSRYSNFLRWVSDGDV 120
DB 61 YYYADAKGFTTISRDNAKNSLYLQMSLAETHAVYYCARDSRYSNFLRWVSDGDV 120
QY 121 WGOGTTIVSS 131
DB 121 WGOGTTIVSS 131
RESULT 2
US-09-240-274-27
; Sequence 27, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) chain E03
US-09-240-274-27
Query Match
Best Local Similarity 100.0%; Score 689; DB 3; Length 131;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 27
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E0115
US-09-240-274-27
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Query Match      93.3%; Score 643; DB 3; Length 127;
Best Local Similarity 95.4%; Pred. No. 1.3e-53;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
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QY 1 EVQLLESGVSGGGLVPPGASLRISCASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
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DB 1 EVQLL-----ESGGGLVPPGASLRISCASGFTFSYSMHWVROGPGKLEWVSSISNSNT 56
QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHYAVYVCARDSRYSNFLRWVRSDGMDV 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 57 YIYADAVKGRFTISRDNKNSLYLQMSLRAEDYAVYVCARDSRYSNFLRWVRSDGMDV 116
QY 121 WGGGTIVYSS 131
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DB 117 WGGGTIVYSS 127
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RESULT 3
US-08-918-148-78
Sequence 78, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W
APPLICANT: Carter, Paul J.
APPLICANT: Pendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO: 78
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
FEATURE:
NAME/KEY: unknown
LOCATION: 208
OTHER INFORMATION: unknown amino acid
US-08-918-148-78
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Query Match      73.7%; Score 507.5; DB 4; Length 245;
Best Local Similarity 77.9%; Pred. No. 1.6e-40;
Matches 102; Conservative 9; Mismatches 7; Indels 13; Gaps 2;
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QY 1 EVQLLESGVSGGGLVPPGASLRISCASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
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DB 3 EVQLL-----VESGGGLVPPGASLRISCASGFTFSYNNMWVROGPGKLEWVSSISNSNT 58
QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHYAVYVCARDSRYSNFLRWVRSDGMDV 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 59 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDYAVYVCARDR-----GSTGMDV 109
QY 121 WGGGTIVYSS 131
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DB 110 WGGGTIVYSS 120
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RESULT 4
US-10-039-785-53
Sequence 53, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunoselectively Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 53
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53
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Query Match      70.8%; Score 488; DB 4; Length 249;
Best Local Similarity 75.8%; Pred. No. 1.1e-38;
Matches 100; Conservative 9; Mismatches 15; Indels 8; Gaps 3;
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DB 1 EVQLL-----ESGGGLVPPGASLRISCASGFTFSYAMSWVROGPGKLEWVSSISNSNT 56
QY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHYAVYVCARDSRYSNFLRWVR--SDGMD 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 57 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDYAVYVCARDR-----PSFOGHWYSYGM 113
QY 120 WGGGTIVYSS 131
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DB 114 WGGGTIVYSS 125
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RESULT 5
US-08-379-057-32
Sequence 32, Application US/08379057
Patent No. 5876950
GENERAL INFORMATION:
APPLICANT: Sladak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jürgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
In Diagnosis and Therapy
```


FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-30

Query Match 69.8%; Score 481; DB 4; Length 123;
Best Local Similarity 76.5%; Pred. No. 2,3e-38;
Matches 101; Conservative 8; Mismatches 13; Indels 10; Gaps 4;

QY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
DB 1 QVQL---VESGGGLVPGGSLRLSCAASGFTFSYEMNVRQAPGKLEWVYISSSGS 56
QY 61 YIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYICARD-SRYSNPLRWVRSDGMD 119
DB 57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRADDTAVYICARDLGTS--YGYV--GLD 111
QY 120 WVGQGTIVYVSS 131
DB 112 WVGQGTIVYVSS 123

RESULT 8
US-08-918-148-75
Sequence 75; Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
TYPE: PRP
ORGANISM: artificial
US-08-918-148-75

Query Match 69.6%; Score 479.5; DB 4; Length 245;
Best Local Similarity 72.5%; Pred. No. 7.1e-38;
Matches 95; Conservative 8; Mismatches 15; Indels 13; Gaps 2;

QY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
DB 3 EVPL---VOSGGGLVPGGSLRLSCAASGFTFSYDMYMWIRQAPGKLEWVYISSSGS 58
QY 61 YIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYICARDSRYSNPLRWVRSDGMDV 120
DB 59 TIYYADSVKGRFTISRDNSKNTLYLQMNSLRADDTAVYICA-----RMSGEDAFDI 109
QY 121 WVGQGTIVYVSS 131
DB 110 WVGQGTIVYVSS 120

RESULT 9
US-08-211-202-134
Sequence 134; Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneerus Jacobus Mattheus
APPLICANT: BAIRER, Michael
APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-134

Query Match 69.4%; Score 478.5; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 3.5e-38;
Matches 97; Conservative 7; Mismatches 7; Indels 13; Gaps 2;

QY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
DB 1 EVOL---VOSGGGLVPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVYISSSSS 56
QY 61 YIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYICARDSRYSNPLRWVRSDGMDV 120
DB 57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRADDTAVYICARS-----VDSYGMGV 107


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RESULT 12
US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil A.
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
; US-08-476-349A-102

Query Match      68.3%; Score 470.5; DB 1; Length 128;
Best Local Similarity 72.7%; Pred. No. 2.4e-37;
Matches 96; Conservative 9; Mismatches 22; Indels 5; Gaps 2;
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QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSSMHWVROGPGKGLEWVSISNSNT 60
Db 1 EVOL----VESGGGLVPGGSLRLSCAASGFTSSYDMNVRQAPKGLEWVYISASG 56

QY 61 YIYYADAVKGRFTISRDNKNSLYIQNSLRAEHTAVYYCARDSRYSNFLRW-VRSDGMD 119
Db 57 YIYYADSVKGRFTISRDNKNSLYIQNSLRAEHTAVYYCARQGPVQLFEMLLPTIGSD 116

QY 120 WVGQGTIVIVSS 131

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Db 117 WVGQGLVTVSS 128

RESULT 13
US-09-025-769B-24
; Sequence 24, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9000
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-09-025-769B-24

Query Match      68.2%; Score 470; DB 4; Length 117;
Best Local Similarity 73.3%; Pred. No. 2.4e-37;
Matches 96; Conservative 5; Mismatches 16; Indels 14; Gaps 2;
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QY 1 EVOLLESVSGGGLVPGGSLRLSCAASGFTSSSMHWVROGPGKGLEWVSISNSNT 60
Db 1 EVOL----VESGGGLVPGGSLRLSCAASGFTSSYDMNVRQAPKGLEWVYISVDG 56

QY 61 YIYYADAVKGRFTISRDNKNSLYIQNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db 57 NTYYADSVKGRFTISRDNKNSLYIQNSLRAEHTAVYYCARD-----RGSGGDY 106

QY 121 WVGQGTIVIVSS 131
Db 107 WVGQGLVTVSS 117

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RESULT 14
US-09-560-198A-2
; Sequence 2, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
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1  APPLICANT: Thompson, Julia E
2  APPLICANT: Lennard, Simon N
3  APPLICANT: Wilton, Alison J
4  APPLICANT: Braddock, Peta SH
5  APPLICANT: Du Fou, Sarah L
6  APPLICANT: McCafferty, John G
7  APPLICANT: Conroy, Louise A
8  APPLICANT: Tempest, Philip R
9  TITLE OF INVENTION: Specific binding members for TGFbeta1
10 FILE REFERENCE: 28111/336520A
11 CURRENT APPLICATION NUMBER: US/09/560,198A
12 CURRENT FILING DATE: 2000-04-28
13 PRIOR APPLICATION NUMBER: US 60/131,983
14 PRIOR FILING DATE: 1999-04-30
15 NUMBER OF SEQ ID NOS: 25
16 SOFTWARE: PatentIn Ver. 2.1
17 SEQ ID NO 2
18 LENGTH: 123
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-560-198A-2

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Query Match	68.2%;	Score 470;	DB 4;	Length 123;
Best Local Similarity	70.2%;	Pred. No. 2.5e-37;		
Matches 92;	Conservative 14;	Mismatches 17;	Indels 8;	Gaps 2

OY	1	EVOALLESECEVEGEGLVYKPCGGSLRLSCAASGFPESSYSMHVWQGPCKGLEWVSINSNT	60
	:	: : : : : : : : : : : : : : :	
Dd	1	QVOL----YQSGGAGVCPGRSLRLSCAASGFPESSYGMHWBQAPOCKGLEWVAVISDGS	56
OY	61	YIYADAVKGFPTLSRDNAKNSLYLOMSSLRAEHAAYVCARDRSNPLRWVRSDGMV	120
	:	: : : : : : : :	
Dd	57	IKTIYADSKGFTLISRDNSKNTLIOMSSLRAEDTAIVYCARTGETSGI---DISGVEL	112
OY	121	WGCGTTVVISS	131
	:	: : :	
Dd	113	WGCGTTVVISS	123

RESULT 15
 ; Sequence 73, Application US/08478039
 ; Patent No. 5681722
 ; GENERAL INFORMATION:
 ; APPLICANT: Newman, Roland A.
 ; APPLICANT: Hanna, Nabil
 ; APPLICANT: Raab, Ronald W.
 ; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 ; NUMBER OF SEQUENCES: 114
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince St.
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22113-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,039
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/379,072
 ; FILING DATE: 25-JAN-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/912,292
 ; FILING DATE: 10-JUL-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/856,281

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1 FILING DATE: 23-MAR-1992
2
3 PRIOR APPLICATION DATA:
4
5 APPLICATION NUMBER: US 07/735,064
6
7 FILING DATE: 25-JUL-1991
8
9 ATTORNEY/AGENT INFORMATION:
10
11 NAME: Teekin Esq., Robin L.
12
13 REGISTRATION NUMBER: 35,030
14
15 REFERENCE/DOCKET NUMBER: 012712-1660
16
17 TELECOMMUNICATION INFORMATION:
18
19 TELEPHONE: 703-836-6620
20
21 TELEFAX: 703-836-2021
22
23 INFORMATION FOR SEQ ID NO: 73:
24
25 SEQUENCE CHARACTERISTICS:
26
27 LENGTH: 128 amino acids
28
29 TYPE: amino acid
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31 STRANDEDNESS: not relevant
32
33 TOPOLOGY: not relevant
34
35 MOLECULE TYPE: peptide
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37 ORIGINAL SOURCE:
38
39 ORGANISM: Monkey
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41 POSITION IN GENOME:
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43 CHROMOSOME/SEGMENT: VHS clone 3-40
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Query Match	68.1%;	Score 469.5;	DB 1;	Length 128;
Best Local Similarity	72.0%;	Pred. No. 2.9e-37;		
Matches	95;	Conservative	10;	Mismatches 22;
			Indels	5;
			Gaps	2

[illegible]

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Job time : 36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2003, 06:29:06 ; Search time 467 Seconds
(without alignments)
42.444 Million cell updates/sec

Title: US-09-848-798a-28
Perfect score: 689
Sequence: 1 EVOLLESGEVESGGGLVKKPGG.....WVRSDGMDVWGQTTIVISS 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	689	100.0	131	US-09-848-798-28	Sequence 28, Appl
2	643	93.3	127	US-09-848-798-27	Sequence 27, Appl
3	511.5	74.2	256	US-09-880-748-1318	Sequence 1318, Ap
4	509	73.9	248	US-09-880-748-913	Sequence 913, Ap
5	506.5	73.5	247	US-09-880-748-1764	Sequence 1764, Ap
6	504.5	73.2	116	US-10-091-300-24	Sequence 24, Appl
7	499.5	72.5	116	US-10-091-300-31	Sequence 31, Appl
8	499.5	72.5	249	US-09-880-748-1856	Sequence 1856, Ap
9	498	72.3	241	US-09-880-748-1937	Sequence 1937, Ap
10	497.5	72.2	247	US-09-880-748-1703	Sequence 1703, Ap
11	495.5	71.9	249	US-09-880-748-974	Sequence 974, Appl
12	494.5	71.8	248	US-09-880-748-1974	Sequence 1974, Appl
13	493.5	71.6	262	US-09-880-748-2081	Sequence 2081, Appl
14	492.5	71.5	252	US-09-880-748-1634	Sequence 1634, Appl
15	491.5	71.3	128	US-09-840-459-77	Sequence 77, Appl

16	491.5	71.3	128	10	US-09-840-459-79	Sequence 79, Appl
17	491	71.3	250	11	US-09-880-748-1179	Sequence 1179, Ap
18	491	71.3	255	11	US-09-880-748-1608	Sequence 1608, Ap
19	489.5	71.0	248	11	US-09-880-748-1965	Sequence 1965, Ap
20	489	71.0	244	11	US-09-880-748-1991	Sequence 1991, Ap
21	488	70.8	249	13	US-10-033-785-53	Sequence 53, Appl
22	487.5	70.8	256	11	US-09-880-748-1209	Sequence 1209, Ap
23	487.5	70.8	258	11	US-09-880-748-1841	Sequence 1841, Ap
24	485.5	70.5	250	11	US-09-880-748-1613	Sequence 1613, Ap
25	485	70.4	127	10	US-09-840-459-87	Sequence 87, Appl
26	484	70.2	255	11	US-09-880-748-1819	Sequence 1819, Ap
27	483	70.1	121	10	US-09-840-459-92	Sequence 92, Appl
28	483	70.1	125	10	US-09-840-459-76	Sequence 76, Appl
29	482.5	70.0	252	11	US-09-880-748-1362	Sequence 76, Appl
30	482.5	70.0	253	12	US-10-120-414-76	Sequence 76, Appl
31	480.5	69.7	237	11	US-09-880-748-2104	Sequence 2104, Appl
32	480.5	69.7	240	11	US-09-880-748-2105	Sequence 2105, Appl
33	480.5	69.7	240	11	US-09-880-748-2113	Sequence 2113, Appl
34	479.5	69.6	126	12	US-10-041-860-13	Sequence 13, Appl
35	479.5	69.6	126	12	US-10-041-860-208	Sequence 208, Appl
36	478.5	69.4	247	11	US-09-880-748-1294	Sequence 1294, Appl
37	478.5	69.4	251	11	US-09-880-748-908	Sequence 908, Appl
38	477.5	69.3	120	11	US-09-995-529-8	Sequence 8, Appl
39	477.5	69.3	126	12	US-10-041-860-270	Sequence 270, Appl
40	477.5	69.3	237	11	US-09-880-748-2020	Sequence 2020, Appl
41	477.5	69.3	444	15	US-10-325-694-144	Sequence 6, Appl
42	477	69.2	138	12	US-10-325-694-144	Sequence 144, Appl
43	477	69.2	138	12	US-10-325-694-150	Sequence 150, Appl
44	476	69.1	243	11	US-09-880-748-2102	Sequence 2102, Appl
45	475.5	69.0	254	11	US-09-880-748-1701	Sequence 1701, Appl

ALIGNMENTS

RESULT 1
US-09-848-798-28
; Sequence 28, Application US/09848798
; Publication No. US20030040605A1
GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798-28
Query Match 100.0%; Score 689; DB 11; Length 131;
Best Local Similarity 100.0%; Pred. No. 8.1e-56;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLLESGEVESGGGLVKKPGGSLRLSCAASGFTSSYSHMWVRQGGKLEWVSISNSNT 60
|||||
Db 1 EVOLLESGEVESGGGLVKKPGGSLRLSCAASGFTSSYSHMWVRQGGKLEWVSISNSNT 60
QY 61 YYYVDAVKGRTTIRDAKNSLYLQNNSLREHRAVYYCCARDSYNSFLRVRSDDMDV 120
|||||
Db 61 YYYVDAVKGRTTIRDAKNSLYLQNNSLREHRAVYYCCARDSYNSFLRVRSDDMDV 120
QY 121 WQGGTTIVISS 131

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Db      121 WGGGTTVTVSS 131

RESULT 2
US-09-848-798-27
; Sequence 27, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: R1(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 0396-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-03-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 127
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E011s
US-09-848-798-27

Query Match      93.3%; Score 643; DB 11; Length 127;
Best Local Similarity 95.4%; Pred. No. 1,3e-51;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

Cy      1 EVOLLESVSGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 60
      1 EVOL-----ESGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 56
Db      61 YIYADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARDRSYRNFLEWVSISNNT 120
      57 YIYADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARDRSYRNFLEWVSISNNT 116
Cy      121 WGGGTTVTVSS 131
      117 WGGGTTVTVSS 127
Db

RESULT 3
US-09-880-748-1318
; Sequence 1318, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1318
; LENGTH: 256
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-880-748-1318

Query Match      74.2%; Score 511.5; DB 11; Length 256;
Best Local Similarity 78.2%; Pred. No. 2.8e-39;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;

Cy      1 EVOLLESVSGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 60
      1 EVOL-----VDSGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 56
Db      61 YIYADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARD--SRYSNLEWVSISNNT 117
      57 YIYADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARDGSEFDITLRLNENYG 116
Cy      118 MDVWGKGTITVVS 130
      117 MDVWGKGTITVVS 129
Db

RESULT 4
US-09-880-748-913
; Sequence 913, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 913
; LENGTH: 248
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-880-748-913

Query Match      73.9%; Score 509; DB 11; Length 248;
Best Local Similarity 78.6%; Pred. No. 4.6e-39;
Matches 103; Conservative 8; Mismatches 14; Indels 6; Gaps 2;

Cy      1 EVOLLESVSGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 60
      1 EVOL-----VESGGGLVPRGSLRLSCAASGFTSSSMHWYRQPGKLEWVSISNNT 56
Db      61 YIYADAVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARDRSYRNFLEWVSISNNT 120
      57 YIYADSVKGRFTISRDNKNSLYLQNSLRAEHTAVYCCARD--DILGYIYYIGLDV 114
Cy      121 WGGGTTVTVSS 131
      115 WGGGTTVTVSS 125
Db

RESULT 5
US-09-880-748-1764
; Sequence 1764, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
```

;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1764
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1764

Query Match 73.5%; Score 506.5; DB 11; Length 247;
Best Local Similarity 78.6%; Pred. No. 7.8e-39;
Matches 103; Conservative 10; Mismatches 11; Indels 7; Gaps 3;

Qy 1 EVOLLESGVSGGLVYKPGGSLRLSCAASGFTFSYSMHWVROGFGKLEWVSSISNSNT 60
Db 1 QVQL---VQSGGGLVYKPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISSSS 56
Qy 61 YIYADAVKGRFTISRDAKNSLYLQMSLRAEHTAVYYCARDKRYSNFLRWVRSDGMV 120
Db 57 YIYADSVKGRFTISRDAKNSLYLQMSLRAEDTAIVYYCARD-ETDILTGLDQ--GMV 113
Qy 121 WGQGTIVYSS 131
Db 114 WGKGTLVYSS 124

RESULT 6
US-10-091-300-24
;; Sequence 24, Application US/10091300
;; Publication No. US20030108545A1
;; GENERAL INFORMATION:
;; APPLICANT: Rockwell, Patricia
;; APPLICANT: Goldstein, Neil I.
;; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
;; FILE REFERENCE: 11245/46211
;; CURRENT APPLICATION NUMBER: US/10/091,300
;; CURRENT FILING DATE: 2002-03-04
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 24
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Human
US-10-091-300-24

Query Match 73.2%; Score 504.5; DB 15; Length 116;
Best Local Similarity 77.1%; Pred. No. 5.3e-39;
Matches 101; Conservative 8; Mismatches 7; Indels 15; Gaps 2;

Qy 1 EVOLLESGVSGGLVYKPGGSLRLSCAASGFTFSYSMHWVROGFGKLEWVSSISNSNT 60
Db 1 EVOL---VQSGGGLVYKPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISSSS 56
Qy 61 YIYADAVKGRFTISRDAKNSLYLQMSLRAEHTAVYYCARDKRYSNFLRWVRSDGMV 120
Db 57 YIYADSVKGRFTISRDAKNSLYLQMSLRAEDTAIVYYCAR-----VTDARDI 105
Qy 121 WGQGTIVYSS 131
Db 106 WGQGTIVYSS 116

RESULT 7

US-10-091-300-31
;; Sequence 31, Application US/10091300
;; Publication No. US20030108545A1
;; GENERAL INFORMATION:
;; APPLICANT: Rockwell, Patricia
;; APPLICANT: Goldstein, Neil I.
;; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
;; FILE REFERENCE: 11245/46211
;; CURRENT APPLICATION NUMBER: US/10/091,300
;; CURRENT FILING DATE: 2002-03-04
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 31
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Human
US-10-091-300-31

Query Match 72.5%; Score 499.5; DB 15; Length 116;
Best Local Similarity 76.3%; Pred. No. 1.5e-38;
Matches 100; Conservative 9; Mismatches 7; Indels 15; Gaps 2;

Qy 1 EVOLLESGVSGGLVYKPGGSLRLSCAASGFTFSYSMHWVROGFGKLEWVSSISNSNT 60
Db 1 EVOL---VQSGGGLVYKPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISSSS 56
Qy 61 YIYADAVKGRFTISRDAKNSLYLQMSLRAEHTAVYYCARDKRYSNFLRWVRSDGMV 120
Db 57 YIYADSVKGRFTISRDAKNSLYLQMSLRAEDTAIVYYCAR-----VTDARDI 105
Qy 121 WGQGTIVYSS 131
Db 106 WGQGTIVYSS 116

RESULT 8
US-09-880-748-1856
;; Sequence 1856, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunologically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1856
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1856

Query Match 72.5%; Score 499.5; DB 11; Length 249;
Best Local Similarity 78.6%; Pred. No. 3.4e-38;
Matches 103; Conservative 7; Mismatches 14; Indels 7; Gaps 3;

Qy 1 EVOLLESGVSGGLVYKPGGSLRLSCAASGFTFSYSMHWVROGFGKLEWVSSISNSNT 60
Db 1 EVOL---VQSGGGLVYKPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISSSS 56
Qy 61 YIYADAVKGRFTISRDAKNSLYLQMSLRAEHTAVYYCARDKRYSNFLRWVRSDGMV 120

Db 57 YIYPAADSVKGRFTISDNKNSLYLQMNLSRAEDTAIYTCAR-GNYDILTQETFS--FDY 113

QY 121 WGQGTIVIVSS 131

Db 114 WGQGTIVIVSS 124

```

RESULT 9
US-09-880-748-1937
? Sequence 1937, Application US/09880748
? Publication No. US20030059937A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
? FILE REFERENCE: PFE23
? CURRENT FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1937
? LENGTH: 241
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-880-748-1937

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Query Match          72.3%; Score 498; DB 11; Length 241;
Best Local Similarity 77.7%; Pred. No. 4,5e-38;
Matches 101; Conservative 7; Mismatches 8; Indels 14; Gaps 2

OY      2 VOLLESGVESGGLVPCPGSLRLSCAASGFPPSSYSMMHWRCGPCKGLEWVSISINNTY 61
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       2 VQL-----VQSGGGLVKSGSGLRSLCAASGFPTFSSYSMMWVRAPKRGLEWVISISSSY 57
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      62 IYYDAVAVGRFTTISDNNAKNLSLYLOMNSLRBHEHTVYVCARPSRNFLRWRSQGMVY 121
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       58 IYYDASVGGRFTTISDNNAKNLSLYLOMNSLRADETVYVCARHFF-----GMDVY 107
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      122 GGCTTVATSS 131
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       108 GRGTMTVTSS 117

RESULT 10
US-09-880-748-1703
Sequence 1703; Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
Applicant: Ruben et al.
TITLE OF INVENTION: Antilodules that Immunospecifically Bind BlyS
FILE REFERENCE: PPS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
```

```

: NUMBER OF SEQ ID NOS: 3239
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1703
: LENGTH: 247
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-860-748-1703

```

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Oy      1  EVOLLESGVEGGGLVPRPGGSLRLSCAASGFTFSYSSMHMWVROQGGKGLIEWYSSITSNSMT 60
Db      1  QVOL-----VEEGGGLVPRPGGSLRLSCAASGFTFSYSSNMWVQAQGGKGLIEWYSSITSSSS 56
Query Match Similarity 72.2%; Score 497.5; DB 11; Length 247;
Best Local Similarity 78.6%; Pred. No. 5,2e-38;
Matches 103; Conservative 8; Mismatches 13; Indels 7; Gaps 3

Oy      121  WGCGTIVYSS 131
Db      114  WGCGTLTVYSS 124
Query Match Similarity 100%; Score 100; DB 11; Length 10;
Best Local Similarity 100%; Pred. No. 1e-05;
Matches 10; Conservative 10; Mismatches 0; Indels 0; Gaps 0

RESULT 11
US-09-880-748-974
; Sequence 974, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Bvys
; FILE REFERENCE: p523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 974
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-974

```

[illegible]

Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1974
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1974

Query Match
Best Local Similarity 71.8%; Score 494.5; DB 11; Length 248;
Matches 100; Conservative 8; Mismatches 14; Indels 9; Gaps 2;

Qy 1 EVQLLESGVSGGGLVPRGSLRLSCAASGFTFSYSMHWVRQPGKGLEWVSISNSNT 60
Db 1 EVQL-----VQSGGGLVPGGSLRLSCAASGFTFSYEMNWRQAPGKGLEWVSISSGS 56
Qy 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDISYFELMWVSDGDV 120
Db 57 TIYADSVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSGRQAYYY-----GMDV 111
Qy 121 WGQGTIVYSS 131
Db 112 WGQGTIVYSS 122

RESULT 13
US-09-880-748-2081
Sequence 2081, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2081
LENGTH: 262
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match
Best Local Similarity 71.6%; Score 493.5; DB 11; Length 262;
Matches 100; Conservative 13; Mismatches 7; Indels 23; Gaps 3;

Qy 1 EVQLLESGVSGGGLVPRGSLRLSCAASGFTFSYSMHWVRQPGKGLEWVSISNSNT 60
Db 1 EVQL-----VQSGGGLVPRGSLRLSCAASGFTITINYSNMWRQAPGKGLEWVSISSSS 56
Qy 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDR-----YSN 108
Db 57 YIYADSVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDFOVWGVFIANPITVNY 116
Qy 109 FLRWVRSMDVWGQGTIVYSS 131
Db 117 Y-----GMDVWGQGTIVYSS 132

RESULT 14
US-09-880-748-1634
Sequence 1634, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1634
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1634

Query Match
Best Local Similarity 71.5%; Score 492.5; DB 11; Length 252;
Matches 100; Conservative 11; Mismatches 9; Indels 17; Gaps 3;

Qy 1 EVQLLESGVSGGGLVPRGSLRLSCAASGFTFSYSMHWVRQPGKGLEWVSISNSNT 60
Db 1 QVQL-----VQSGGGLVPGGSLRLSCAASGFTFSYSMNWRQAPGKGLEWVSISRSSR 56
Qy 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARD-----SRYSNPLRWVR 114
Db 57 TIYADSVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDRDYDILTYSNY----- 111
Qy 115 SDGMDVWGQGTIVYSS 131
Db 112 --GMDVWGQGTIVYSS 126

RESULT 15
US-09-840-459-77
Sequence 77, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012

Wed Sep 24 09:31:29 2003

us-09-848-798a-28.rapb

Page 6

;; CURRENT APPLICATION NUMBER: US/09/840,459
;; CURRENT FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: PCT/US01/03537
;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: 09/497,625
;; PRIOR FILING DATE: 2000-02-03
;; PRIOR APPLICATION NUMBER: 09/359,193
;; PRIOR FILING DATE: 1999-07-22
;; PRIOR APPLICATION NUMBER: 09/121,781
;; PRIOR FILING DATE: 1998-07-23
;; NUMBER OF SEQ ID NOS: 107
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 77
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: (1)..(128)
;; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-840-459-77

Query Match 71.3%; Score 491.5; DB: 10; Length 128;
Best local similarity 75.4%; Pred. No. 9.1e-38;
Matches 101; Conservative 8; Mismatches 16; Indels 9; Gaps 3;
QY 1 EVQLLESGVESGGLVPRGSGLRISCAASGFTSSISMHWYRQCGPKGLEWYSISNSNT 60
Db 1 EVQLLESGVESGGLVPRGSGLRISCAASGFTSSISMHWYRQCGPKGLEWYSISNSNT 60
QY 61 YYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYICARDISYSNFLRWRS--DG 117
Db 57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARDIRNYDF--WSGYXXYYG 114
QY 118 MDVWGQGTIVVSS 131
Db 115 MDVWGQGTIVVSS 128

Search completed: September 24, 2003, 06:46:03
Job time : 467 secs


```
OY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
OY 121 WGQGTIVIVSS 131
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 121 WGQGTIVIVSS 131
```

```
RESULT 2
US-09-848-798-28
; Sequence 28, Application US/09848798
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798-28
```

```
Query Match 100.0%; Score 689; DB 23; Length 131;
Best Local Similarity 100.0%; Pred. No. 1,9e-62;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
OY 121 WGQGTIVIVSS 131
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 121 WGQGTIVIVSS 131
```

```
RESULT 3
US-09-848-798a-28
; Sequence 28, Application US/09848798a
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798a
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: 1999-05-02
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798a-28
Query Match 100.0%; Score 689; DB 23; Length 131;
Best Local Similarity 100.0%; Pred. No. 1,9e-62;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
OY 121 WGQGTIVIVSS 131
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 121 WGQGTIVIVSS 131
```

```
RESULT 4
US-09-791-537-71782
; Sequence 71782, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71782
; LENGTH: 127
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-71782
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Query Match 93.3%; Score 643; DB 22; Length 127;
Best Local Similarity 95.4%; Pred. No. 1e-57; 2; Indels 4; Gaps 1;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
OY 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 1 EVOLLESGVSGGLVPGGSLRLSCAASGFTFSYSMHWROGPGKLEWVSISNSNT 60
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 120
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARDSTRSNFLRWVRSDGMDV 116
OY 121 WGQGTIVIVSS 131
;
; FEATURe:
; OTHER INFORMATION: anti-Rh(D) chain E03
Db 117 WGQGTIVIVSS 127
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RESULT 5
US-09-848-798-27
; Sequence 27, Application US/09848798
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
```

; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E011s
US-09-848-798-27

Query Match 93.3%; Score 643; DB 23; Length 127;
Best Local Similarity 95.4%; Pred. No. 1e-57;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

OY 1 EVOLLESGVSGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 60
Db 1 EVQLL-----ESGGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSRYSNFLRWVRSDGMDV 120
Db 57 YIYADAVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARSRYSNFLRWVRSDGMDV 116
OY 121 WGQGTIVYSS 131
Db 117 WGQGTIVYSS 127

RESULT 6

US-09-848-798a-27
; Sequence 27, Application US/09848798A
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: 1999-05-02
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E011s
US-09-848-798a-27

Query Match 93.3%; Score 643; DB 23; Length 127;
Best Local Similarity 95.4%; Pred. No. 1e-57;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

OY 1 EVOLLESGVSGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 60
Db 1 EVQLL-----ESGGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSRYSNFLRWVRSDGMDV 120
Db 57 YIYADAVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARSRYSNFLRWVRSDGMDV 116
OY 121 WGQGTIVYSS 131
Db 117 WGQGTIVYSS 127

RESULT 7

US-09-791-537-88960
; Sequence 88960, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88960
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-88960

Query Match 76.2%; Score 525; DB 22; Length 145;
Best Local Similarity 80.9%; Pred. No. 1.7e-45;
Matches 106; Conservative 7; Mismatches 12; Indels 6; Gaps 2;

OY 1 EVOLLESGVSGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 60
Db 20 EVQL-----VESGGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISSSSS 75
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARSRYSNFLRWVRSDGMDV 120
Db 76 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDVEATVTYY--GMDV 133
OY 121 WGQGTIVYSS 131
Db 134 WGQGTIVYSS 144

RESULT 8

US-09-791-537-96307
; Sequence 96307, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96307
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-96307

Query Match 75.9%; Score 523; DB 22; Length 134;
Best Local Similarity 79.7%; Pred. No. 2.5e-45;
Matches 106; Conservative 7; Mismatches 14; Indels 6; Gaps 2;

OY 1 EVOLLESGVSGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISNSNT 60
Db 1 EVQL-----VESGGGLVKKPGGSLRLSCAASGFTFSYSMHWVROGPKGLEWVSISSSSS 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRAEHTAVYYCARS--YSNFLRWVRSDGM 118
Db 57 YIYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARGGLLPELLELLSYYYGYM 116
OY 119 DWGQGTIVYSS 131
Db 117 DWGQGTIVYSS 129

RESULT 9

US-09-791-537-39928
; Sequence 39928, Application US/09791537
; GENERAL INFORMATION:

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; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39928
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-39928
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```

Query Match          74.5%; Score 513.5; DB 22; Length 148;
Best Local Similarity 80.2%; Pred. No. 2,6e-44;
Matches 105; Conservative 7; Mismatches 10; Indels 9; Gaps 3;
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OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROGPGKLEWVSSISNSNT 60
    ||||| 1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 20 EVOL----VESGGGLVPGGSLRLSCAASGFTFSYSMMHWVROAPGKLEWVSSISSSS 75
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDKRSNFKLRVRSDDGV 120
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 76 YIYADSVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDLNG---OML-VQGEDY 130
OY 121 WGGGTLTVIVSS 131
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 131 WGGGTLTVIVSS 141
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RESULT 10
US-09-791-537-90526
; Sequence 90526, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Derek
; APPLICANT: Debe, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90526
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-90526
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Query Match          74.2%; Score 511.5; DB 22; Length 128;
Best Local Similarity 80.5%; Pred. No. 3,6e-44;
Matches 107; Conservative 7; Mismatches 12; Indels 7; Gaps 3;
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```

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROGPGKLEWVSSISNSNT 60
    ||||| 1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 1 EVOL----VESGGGLVPGGSLRLSCAASGFTFSYSMMHWVROAPGKLEWVSSISSSS 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDKRSNFKLRVRSDDGV 118
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 57 YIYADSVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDNYDSSGSLRRYYY-CM 115
OY 119 DVMGGGTLTVIVSS 131
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 116 DVMGGGTLTVIVSS 128
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```

RESULT 11
PCT-US01-19110-1318
; Sequence 1318, Application PC/TUS0119110
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; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PE523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1318
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1318
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Query Match          74.2%; Score 511.5; DB 1; Length 256;
Best Local Similarity 78.2%; Pred. No. 8,2e-44;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;
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```

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROGPGKLEWVSSISNSNT 60
    ||||| 1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 1 EVOL----VOSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROAPGKLEWVSSISSSS 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRADETAVYYCARD-SRYSNFKLRVRSDD--G 117
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 57 YIYADSVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDLGSFYDILTRLENYG 116
OY 118 MDVWGGGTLTVIVS 130
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 117 MDVWGGGTLTVIVS 129
```

```

RESULT 12
PCT-US02-36496-1318
; Sequence 1318, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PE523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1318
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1318
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```

Query Match          74.2%; Score 511.5; DB 1; Length 256;
Best Local Similarity 78.2%; Pred. No. 8,2e-44;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;
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```

OY 1 EVOLLESGVSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROGPGKLEWVSSISNSNT 60
    ||||| 1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 1 EVOL----VOSGGGLVPGGSLRLSCAASGFTFSYSMMHWVROAPGKLEWVSSISSSS 56
OY 61 YIYADAVKGRFTISRDNKNSLYLQMSLRADETAVYYCARD-SRYSNFKLRVRSDD--G 117
    |||||1:|||||1:|||||1:|||||1:|||||1:|||||1:|||||1:
Db 57 YIYADSVKGRFTISRDNKNSLYLQMSLRADETAVYYCARDLGSFYDILTRLENYG 116
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 06:27:35; Search time 90 Seconds
(without alignments)
37,475 Million cell updates/sec

Title: US-09-848-798a-28

Perfect score: 689
Sequence: 1 EVQLLESGVSGGGLVPRG.....WVRSDGMDVWGQGTIVVSS 131

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 120229 segs, 25746487 residues

Total number of hits satisfying chosen parameters: 120229

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US12_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507.5	73.7	245	US-09-138-091A-76	Sequence 76, Appl
2	507	73.6	123	PCF-US03-21304-56	Sequence 56, Appl
3	488	70.8	249	PCF-US03-25457-53	Sequence 53, Appl
4	479.5	69.6	245	US-09-138-091A-73	Sequence 73, Appl
5	477.5	69.3	444	US-10-645-215-6	Sequence 6, Appl
6	475	68.9	247	PCF-US03-23826-44	Sequence 44, Appl
7	463	67.2	143	US-10-469-304-17	Sequence 17, Appl
8	463	67.2	474	PCF-US02-26584-3	Sequence 3, Appl
9	460	66.8	113	US-09-723-752B-11	Sequence 11, Appl
10	458	66.5	131	PCF-US03-15937-53	Sequence 53, Appl
11	457.5	66.4	124	US-10-031-722A-2	Sequence 2, Appl
12	454.5	66.0	223	PCF-US03-26779-46	Sequence 46, Appl
13	454.5	66.0	223	PCF-US03-26744-90	Sequence 90, Appl
14	454.5	66.0	223	US-60-485-404-46	Sequence 46, Appl
15	453	65.7	145	PCF-US03-26232-146	Sequence 146, Appl
16	452	65.6	121	PCF-US03-22566-2	Sequence 2, Appl
17	450	65.3	119	PCF-US03-26779-49	Sequence 49, Appl
18	449	65.2	228	PCF-US03-26744-93	Sequence 93, Appl
19	449	65.2	228	PCF-US03-26744-93	Sequence 93, Appl
20	449	65.2	228	US-60-485-404-49	Sequence 49, Appl
21	446	64.7	117	PCF-US03-25161-18	Sequence 18, Appl
22	441	64.0	119	PCF-US03-11113-10	Sequence 10, Appl
23	441	64.0	119	PCF-US03-11113-16	Sequence 16, Appl
24	439.5	63.8	245	US-09-138-091A-74	Sequence 74, Appl
25	438.5	63.6	116	PCF-US03-10749A-14	Sequence 14, Appl
26	438.5	63.6	242	US-09-538-038A-2351	Sequence 2351, Ap

27	438.5	63.6	446	1	PCF-US03-10749A-38	Sequence 38, Appl
28	437	63.4	117	1	PCF-US03-21304-57	Sequence 57, Appl
29	435	63.1	117	1	PCF-US03-21304-59	Sequence 59, Appl
30	435	63.1	239	5	US-09-538-038A-2353	Sequence 2353, Ap
31	434	63.0	117	1	PCF-US03-21304-58	Sequence 58, Appl
32	433.5	62.9	122	6	US-10-031-722A-6	Sequence 6, Appl
33	432	62.7	117	6	US-10-257-864A-99	Sequence 99, Appl
34	432	62.7	136	6	US-10-257-864A-102	Sequence 102, Appl
35	432	62.7	244	5	US-09-138-091A-75	Sequence 75, Appl
36	432	62.7	266	6	US-10-257-864A-108	Sequence 108, Appl
37	431	62.6	123	1	PCF-US03-19333-38	Sequence 38, Appl
38	431	62.6	246	1	PCF-US03-19333-24	Sequence 24, Appl
39	430.5	62.5	124	5	US-09-610-551B-63	Sequence 63, Appl
40	430	62.4	121	1	PCF-US03-22566-10	Sequence 10, Appl
41	429	62.3	246	1	PCF-US03-19333-23	Sequence 23, Appl
42	427.5	62.0	460	1	PCF-US03-23735-5	Sequence 5, Appl
43	426.5	61.9	120	1	PCF-US02-34154-7	Sequence 7, Appl
44	426.5	61.9	120	6	US-10-456-092A-7	Sequence 7, Appl
45	426.5	61.9	122	6	US-10-031-722A-10	Sequence 10, Appl

ALIGNMENTS

```
RESULT 1
US-09-138-091A-76
; Sequence 76, Application US/09138091A
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138, 091A
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056, 736
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scfv) fragments
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-138-091A-76
Query Match 73.7%; Score 507.5; DB 5; Length 245;
Best Local Similarity 77.9%; Pred. No. 9, 6e-35;
Matches 102; Conservative 9; Mismatches 7; Indels 13; Gaps 2;
OY 1 EVQLLESGVSGGGLVPRGSLRSCAAGFTFSYSMMHVRGPGKGLHWSSISNSNT 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 QVQL-----VESGGGLVPRGSLRLSCAAGFTFSINMMWVQAPKGLHWSSISSSS 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 YYYADAVKGRFTISDNKNSLYIQMNSLRHETAVYVYCARDRSYNFLRWVRSDGMDV 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 YYYADAVKGRFTISDNKNSLYIQMNSLRHETAVYVYCARDR-----GSTGMDV 109
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 WGQGTIVVSS 131
||:| | | | |
Db 110 WGRGLTVVSS 120
||:| | | | |
RESULT 2
PCF-US03-21304-56
; Sequence 56, Application PC/TUS0321304
; GENERAL INFORMATION:
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
FILE REFERENCE: 053893-5050MO
CURRENT APPLICATION NUMBER: PCT/US03/21304
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,356
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-21304-56
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Query Match
Best Local Similarity 73.6%; Score 507; DB 1; Length 123;
Matches 105; Conservative 8; Mismatches 9; Indels 10; Gaps 4;
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QY 1 EVOLLESGVSGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1 EVOL---VESGGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISSSS 56
QY 61 YIYDAVAKGRTTISRDNKNSLYLOMNSLRAEHTAVYYCARDSRYSNFLRWVRSQGM-D 119
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 57 YIYADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCARD--HPNY---YDSSGLFD 111
QY 120 WVGQGTIVYSS 131
    |||  |||  |||
DB 112 WVGQGTIVYSS 123
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RESULT 3
PCT-US03-25457-53
Sequence 53, Application PC/TUS0325457
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550PCT2
CURRENT APPLICATION NUMBER: PCT/US03/25457
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: 60/468,050
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/425,730
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/403,382
PRIOR FILING DATE: 2002-08-15
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 53
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1006F07 scfv
PCT-US03-25457-53
```

```
Query Match
Best Local Similarity 70.8%; Score 488; DB 1; Length 249;
Matches 100; Conservative 9; Mismatches 15; Indels 8; Gaps 3;
```

```
QY 1 EVOLLESGVSGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1 EVOLTL---ESGGGLVPRGSLRLSCAASGFTFSYAMSWVROAGKLEWVSAISGSGG 56
QY 61 YIYDAVAKGRTTISRDNKNSLYLOMNSLRAEHTAVYYCARDSRYSNFLRWVRSQGM-D 119
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 57 STIYADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCARD---PSFQOMGHYSYGM 113
QY 120 WVGQGTIVYSS 131
```

```
DB 114 WVGQGTIVYSS 125
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

```
RESULT 4
US-09-138-091A-73
Sequence 73, Application US/09138091A
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 9491-013-27
CURRENT APPLICATION NUMBER: US/09/138,091A
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: US 60/056,736
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 73
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: single chain antibody (scfv) fragments
US-09-138-091A-73
```

```
Query Match
Best Local Similarity 69.6%; Score 479.5; DB 5; Length 245;
Matches 95; Conservative 8; Mismatches 15; Indels 13; Gaps 2;
```

```
QY 1 EVOLLESGVSGGLVPRGSLRLSCAASGFTFSYSMHWVROGPGKLEWVSSISNSNT 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 3 EVOL---VSGGGLVPRGSLRLSCAASGFTFSYMSWVROAGPGKLEWVSYISSSGS 58
QY 61 YIYDAVAKGRTTISRDNKNSLYLOMNSLRAEHTAVYYCARDSRYSNFLRWVRSQGM-D 120
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 59 TIYADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCA-----RMSGEDAFDI 109
QY 121 WVGQGTIVYSS 131
    |||  |||  |||
DB 110 WVGQGTIVYSS 120
```

```
RESULT 5
US-10-645-215-6
Sequence 6, Application US/10645215
GENERAL INFORMATION:
APPLICANT: Adolf, Guenther
APPLICANT: Baum, Anke
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunocjugates and
FILE REFERENCE: 1/1383
CURRENT APPLICATION NUMBER: US/10/645,215
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR FILING DATE: August 21, 2002
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanised Murine Antibody Biwa 4 Heavy Chain
US-10-645-215-6
```

```
Query Match
Best Local Similarity 69.3%; Score 477.5; DB 6; Length 444;
```

Best Local Similarity 72.5%; Pred. No. 4.4e-32;
Matches 95; Conservative 7; Mismatches 12; Indels 17; Gaps 2;

```
OY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSMHWYRQGGKLEWVSSISNNT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVOL---VESGGGLVYKPGGSLRLSCAASGFTFSYDMSWYRQAGKGLEWVSTISSGS 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 YYYADAVKGRFTISRDNKAKNSLYLQMSLRAEHTAVYYCARDSTRYSNPLRWVRSQMDV 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 YTYVDSYKGRFTISRDNKAKNSLYLQMSLRAEDTAVYYCAR-----QGIDY 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 WGQGTIVYSS 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 WGRGTLVTVSS 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 6

PCT-US03-23826-44
; Sequence 44, Application PC/TUS0323826
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against C3a Receptor
; FILE REFERENCE: PF58PCT
; CURRENT APPLICATION NUMBER: PCT/US03/23826
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 60/400,057
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 44
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: D185G07 scfv
PCT-US03-23826-44

Query Match

Best Local Similarity 72.3%; Pred. No. 4.3e-32;
Matches 94; Conservative 10; Mismatches 16; Indels 10; Gaps 2;

```
OY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSMHWYRQGGKLEWVSSISNNT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVOL---VESGGGLVYKPGGSLRLSCAASGFTFSYDMSWYRQAGKGLEWVSTISSGS 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 YYYADAVKGRFTISRDNKAKNSLYLQMSLRAEHTAVYYCARDSTRYSNPLRWVRSQMDV 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 YTYVDSYKGRFTISRDNKAKNSLYLQMSLRAEDTAVYYCARGPDIYST-----DARDI 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 WGQGTIVYSS 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 WKGTLVTVSS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 7

US-10-469-304-17
; Sequence 17, Application US/10469304
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-304-17

Query Match

67.2%; Score 463; DB 6; Length 143;

Best Local Similarity 71.8%; Pred. No. 2.5e-31;
Matches 94; Conservative 8; Mismatches 21; Indels 8; Gaps 2;

```
OY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSMHWYRQGGKLEWVSSISNNT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVOLL---ESGGGLVYKPGGSLRLSCAASGFTFSYAMTWYRQAGKGLEWVSGISGGD 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 YYYADAVKGRFTISRDNKAKNSLYLQMSLRAEHTAVYYCARDSTRYSNPLRWVRSQMDV 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 STYVDSYKGRFTISRDNKAKNSLYLQMSLRAEDTAVYYCARDHSGSYTP-----WFDY 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 WGQGTIVYSS 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132 WQGTIVTVSS 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 8

PCT-US02-26584-3
; Sequence 3, Application PC/TUS0226584
; GENERAL INFORMATION:
; APPLICANT: HOOVER, Craig
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110 PC
; CURRENT APPLICATION NUMBER: PCT/US02/26584
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-26584-3

Query Match

Best Local Similarity 71.8%; Pred. No. 7.1e-31;
Matches 94; Conservative 11; Mismatches 20; Indels 6; Gaps 2;

```
OY 1 EVOLLESGVESGGGLVYKPGGSLRLSCAASGFTFSYSMHWYRQGGKLEWVSSISNNT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVOLL---ESGGGLVYKPGGSLRLSCAASGFTFSYAMTWYRQAGKGLEWVSAISAGH 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 YYYADAVKGRFTISRDNKAKNSLYLQMSLRAEHTAVYYCARDSTRYSNPLRWVRSQMDV 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 STYVDSYKGRFTISRDNKAKNSLYLQMSLRAEDTAVYYCARDREVIMIV--VLNGPFDY 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 WGQGTIVYSS 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 134 WQGTIVTVSS 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 9

US-09-723-752B-11
; Sequence 11, Application US/09723752B
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

MEDION TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,752B
FILING DATE: 27-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-723-752B-11

```

Query Match	66.8%	Score 460	DB 5	Length 113
Best Local Similarity	71.6%	Pred. No. 3.6e-31		
Matches	94	Conservative	5	Mismatches 14; Indels 18; Gaps 2
QY	1	EVOLLESGVSGGGGLVYPGGSLRLSCAASGTFESYSMMHWVRQPGKGLPMYSINSMNT	60	
Db	1	EVOL-----VESGGGLVQPGSSLRSLSCAASGTFESYSMSNRQAPFGKGLPMYSIVISGDSG	56	
QY	61	YIYIDAVKAGRTTIRDNAAKNSLYLQNNKSLAEHTAVYYCARDQRYSNFLRWRSQMDV	120	
Db	57	STYIDAVKAGRTTIRDNNSKNLTLYLQNNKSLAEHTAVYYCAR-----GFDFY	102	
QY	121	WGQGTTLVTVSS	131	
Db	103	WGQGTTLVTVSS	113	

```

RESULT 10
PCT-US03-15937-53
; Sequence 53, Application PC/TUS0315937
; GENERAL INFORMATION:
; APPLICANT: Hematech, LLC et al.
; TITLE OF INVENTION: Transgenic ungulates Capable of Human
; FILE REFERENCE: 50195/012W02
; CURRENT APPLICATION NUMBER: PCT/US03/15937
; PENDING APPLICATION NUMBER: 2003-07-28381, 531
; PRIOR FILING DATE: 0002-05-17, 60/431, 056
; PRIOR APPLICATION NUMBER: US 60/425, 056
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 131
; TYPE: PRF
; ORGANISM: Bovine
; CCT-US03-15937-53

```

```

Query Match 66.5% Score 458; DB 1; Length 131;
Best Local Similarity 74.8%; Pred. No. 6e-31;
Matches 89; Conservative 6; Mismatches 14; Indels 10; Gaps 1.

OY 13 GGLVPGSLRLSCASGFFPSSYSMMVWQPGKGLIEWSSISNSNTIYYADANKGF 72
|||||

```

Db 1 GGIVKPGGSLRLSCAAGSGLFEEFSDYYSMTIRQAGCKLEWVSYISSGSIYYADSVKGRF 60

Qy 73 TISRDAKNSLYIQMNSLRAEHTAAVYYCAARDKSYNFLMNVSDGDDGGQGTIVYS 111

Db 61 TISRDAKNSLYIQMNSLRAEHTAAVYYCAARDKSYNFLMNVSDGDDGGQGTIVYS 109

```

RESULT 11
US-10-031-722A-2
Sequence 2, Application US/10031722A
GENERAL INFORMATION:
APPLICANT: Medarex, Inc.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU
FILE REFERENCE: MX1-160PC
CURRENT APPLICATION NUMBER: US/10/031,722A
CURRENT FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: USSN 60/146,313
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: USSN 60/188,539
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-10-031-722A-2

```

Query Match	Similarity	Score	457.5	DB	6	Length	124
Best	Local	Similarity	71.0%	pred	No.	6,2e-31	
Matches	93	Conservative	10	Mismatches	21	Indels	7
						Gaps	2
QY	1	EVOLLESGVSGGGLYKRGSGSLRLSCAAGSTFSSYMHVYRQGPCKGLEMYSTNSMT	60				
QY	1	EVQLL-----ESGGGLVQPGSSLRISCAAGSTFSSIMTWYKAPGKGLKEMYSALISGSG	56				
Db							
QY	61	YIYYADAVKAGRTTISRDNAKNSLYLQNNSLRAEHTAVYTCARDSRYSNFLRWYRSGMDY	120				
QY	57	STFYVADSEGGRTTISRDNKNTLYLQNNSLRAEHTAVYTCAKGPGYSGSYTH--FDY	113				
Db							
QY	121	WGQGTFTVIVSS	131				
QY	114	WGQGTFTVIVSS	124				

```

RESULT 12
PCT-US03-26779-46
? Sequence 46, Application PC/TU030326779
? GENERAL INFORMATION:
? APPLICANT: Prior, Christopher P.
? APPLICANT: Turner, Andrew J.
? APPLICANT: Sadeghi, Homayoun
? TITLE OF INVENTION: Transferrin Fusion Protein Libraries
? FILE REFERENCE: 054710-5007-WO
? CURRENT APPLICATION NUMBER: PCT/US03/26779
? CURRENT FILING DATE: 2003-08-26
? PRIOR APPLICATION NUMBER: US 60/406,977
? PRIOR FILING DATE: 2002-08-30
? PRIOR APPLICATION NUMBER: US 10/384,060
? PRIOR FILING DATE: 2003-03-10
? PRIOR APPLICATION NUMBER: US 60/485,404
? PRIOR FILING DATE: 2003-07-09
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 46
? LENGTH: 223
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No.
? C1: US03-26779-46

```

Query Match	66.0%:	Score 454.5:	DB 1:	Length 223:
Best Local Similarity	70.2%:	Pred. No. 1.8e-30:		
Matches	92:	Conservative 10:	Mismatches 16:	Indels 13:
			Gaps 2:	
QY	1	EVOLLSEGVESGGGLVYKPGGSLRLSCA	SGFTFSYSMHWYKPGKGLIEWVSSISNSNT	60
				:
				:
Db	1	QVOLL-----ESGGGVYQPGRSRLRLSCA	SGFTFSYSGHWWYQAGKGLIEWVAIVSYGDS	56
				:
				:
QY	61	YIYADAVKGGFTTISRDNAAKNSLYLQNS	LAERTAYYYCARDSTRYSNPLKRWVSDGMDY	120
				:
				:
Db	57	NKRYADSKGGFTTISRDNKSNKNTLYLQNS	LAEREDVAIVYYCAKDSGLAF-----DI	107
				:
				:
QY	121	WGQGTIVIVSS	131	
Db	108	WGQGTIVIVSS	118	

```

RESULT 13
PCT-US03-26744-90
: Sequence 90, Application PC/TUS0326744
: GENERAL INFORMATION:
: APPLICANT: SADEGHI, Homayoun
: APPLICANT: PRIOR, Christopher P.
: APPLICANT: TURNER, Andrew
: TITLE OF INVENTION: MODIFIED TRANSFERLIN-ANTIBODY FUSION PROTEINS
: FILE REFERENCE: 54710-5004-NO
: CURRENT APPLICATION NUMBER: PCT/US03/26744
: CURRENT FILING DATE: 2003-08-28
: PRIOR APPLICATION NUMBER: US 60/406,977
: PRIOR FILING DATE: 2002-08-30
: PRIOR APPLICATION NUMBER: US 10/384,060
: PRIOR FILING DATE: 2003-03-10
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 90
: LENGTH: 223
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No. BAB18250
PCT-US03-26744-90

```

```

; RESULT 14
; US-60-485-404-46
; Sequence 46, Application US/60485404
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-PR
; CURRENT APPLICATION NUMBER: US/60/485,404
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 10/7231,494
; PRIOR FILING DATE: 2002-08-30

```

```

: PRIOR APPLICATION NUMBER: US 60/406,997
: PRIOR FILING DATE: 2002-08-30
: PRIOR APPLICATION NUMBER: US 10/384,060
: PRIOR FILING DATE: 2003-03-10
: PRIOR APPLICATION NUMBER: US 60/460,829
: PRIOR FILING DATE: 2003-04-08
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 46
: LENGTH: 223
: TYPE: prt
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/key: misc_feature
: OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No. BAB18250
US-60-485-404-46

```

	Query Match	66.0%;	Score 454.5;	DB 7;	Length 223;
	Best Local Similarity	70.2%;	Pred. No. 1,8e-30;		
	Matches	92;	Conservative 10;	Mismatches 16;	Indels 13; Gaps 2
QY	1 EVOLLESGVESGGGIVPKDGSILRLSCAASGFETSSYSMHWRÖPGKGLIEWYSISNSNT 60	: : : : : : : : : :			
Dd	1 QVOLL----ESGGGVYPGRSRLRISCASGFTFSSTGYGMHWRAQAKGKGLEWAVSYSDGS 56	: : : : : : : : : :			
QY	61 YYYADAVKGGFTTSRDNAKNSLYIQANSLRAEHTAVYYCARDSKYSNFLRWVRSDGMV 120	: : : : : : : : : :			
Dd	57 NKRYADVSKGGFTTSRDNSKNLTLYLQNSSLRAEDTAVYYCAKDSDLAF-----DI 107	: : : : : : : : : :			
QY	121 WGGGTIVTVSS 131				
Dd	108 WGCGTNMTVSS 118				

```

RESULT 15
PCT-US03-26232-146
: Sequence 146, Application PC/TUS0326232
: GENERAL INFORMATION:
: APPLICANT: ABGENIX, INC.
: APPLICANT: GUDAS, Jean M.
: APPLICANT: HAAK-FREDSCHO, Mary
: APPLICANT: POORD, Orit
: APPLICANT: LIANG, Meina L.
: APPLICANT: AHUMALIA, Kiran
: APPLICANT: BHAKTA, Sunil
: TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
: TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
: FILE REFERENCE: ABGENIX.091VPC
: CURRENT APPLICATION NUMBER: PCT/US03/26232
: CURRENT FILING DATE: 2003-08-19
: PRIOR APPLICATION NUMBER: US 60/404,802
: PRIOR FILING DATE: 2002-08-19
: NUMBER OF SEQ ID NOS: 149
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 146
: LENGTH: 145
: TYPE: PRT
: ORGANISM: Homosapien
PCT-US03-26232-146

```

Query Match	65.7%	Score 453	DB 1	Length 145
Best Local Similarity	73.8%	Pred. No. 1.7e-30		
Matches	90	Conservative 10	Mismatches 16	Indels 6
				Gaps 2
QY	10	ESGGGIVPGGSLRLSCAAGFTFSSYEMHWROGPGKLEWVSSISNSGTITYYADAVK	69	
		:		
Db	2	QSGGGVVOGPGSLRLSCAAGFTFSSYGMHWYKQAPGKLEWVAIVITDGNKKITYADSVK	61	
QY	70	GRFTISRDNANNSLYLQNSLRAETHAYYCCARDRSYNFLMRVSDGMDVWGQGTIVY	129	
		:		
Db	62	GRFTISRDTSNKFTLYLQNSLRAEDTAYYICARDS--SYIYIY-----GMDVWGQGTIVY	115	
QY				
	130	SS 131		

Wed Sep 24 09:31:30 2003

us-09-848-798a-28.rapn

Page 6

Db 116 SS 117

Search completed: September 24, 2003, 06:38:05
Job time : 90 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2003, 22:39:53 ; Search time 2208 Seconds

(without alignments)
7281.469 Million cell updates/sec

Title: US-09-848-798A-97

Perfect score: 393
Sequence: 1 gaggtgagctgcgtcagtc.....ccacgltcatcgtctcctca 393

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 60 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_un:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	393	100.0	393	6	ARI60968	ARI60968 Sequence
2	393	100.0	393	12	AF044446	AF044446 Synthetic
3	363.6	92.5	381	6	ARI60967	ARI60967 Sequence
4	363.6	92.5	381	12	AF044445	AF044445 Synthetic
5	306	77.9	435	9	HSa234196	AJ234196 Homo sapi
6	296.2	75.4	396	9	HSa519295	AJ519295 Homo sapi
7	294	74.8	378	9	AB066972	AB066972 Homo sapi
8	293.6	74.7	435	9	AF062202	AF062202 Homo sapi
9	293.2	74.6	402	9	HSa389193	AJ389193 Homo sapi
10	291.6	74.2	378	9	HSa519292	AJ519292 Homo sapi
11	288.2	73.3	384	9	HSU77374	U77374 Homo sapi
12	286.6	72.9	385	9	HUWH3H	D83682 Human mRNA
13	284.8	72.5	438	9	AF032350	AF032350 Homo sapi
14	284	72.3	372	9	AF170095	AF170095 Homo sapi
15	283	72.0	387	9	HSa555251	AJ555251 Homo sapi
16	279.6	71.1	375	9	AF174081	AF174081 Homo sapi
17	278.8	70.9	389	9	HSY12442	Y12442 H.sapiens I
18	278.6	70.9	384	9	AF466106	AF466106 Homo sapi
19	278.6	70.9	384	9	AF466107	AF466107 Homo sapi
20	278.6	70.9	441	9	HSR09221	X81751 H.sapiens r
21	278	70.7	429	9	AY190818	AY190818 Homo sapi
22	277.2	70.5	378	9	HSa271554	AJ271554 Homo sapi
23	277.2	70.5	381	9	U00501	U00501 Human immun
24	277.2	70.5	524	9	HUWIGH2I	L29155 Human immun
25	276	70.2	363	9	AY033254	AY033254 Homo sapi
26	275.4	70.1	432	9	HUWIGH3AA	L08082 Human (clon
27	274.8	69.9	339	9	HUWH3L	D83686 Human mRNA
28	274.8	69.9	372	9	HSU77372	U77372 Homo sapi
29	274.4	69.8	357	9	U00572	U00572 Human immun
30	274.2	69.8	357	9	AB063691	AB063691 Homo sapi
31	274	69.7	387	9	HSU80144	U80144 Human immun
32	273.2	69.5	392	9	AF052523	AF052523 Homo sapi
33	273	69.5	488	9	HSIG488	X61014 Human Immun
34	272.2	69.3	339	9	HSWHD007	Z68351 H.sapiens r
35	272.2	69.3	519	6	BD013945	BD013945 Humanized
36	272.2	69.3	519	9	HUWIGH321X	M99658 Human immun
37	272.2	69.3	200000	9	AB019439	AB019439 Homo sapi
38	272.2	69.3	227353	2	AC141259	AC141259 Homo sapi
39	271.8	69.2	375	6	AX061434	AX061434 Sequence
40	271.6	69.1	372	9	HSU95238	U95238 Human clone
41	271.6	69.1	388	9	HSa389186	AJ389186 Homo sapi
42	271.6	69.1	458	9	HSE5432	Z14212 H.sapiens r
43	271.4	69.1	358	9	HSa556823	AJ556823 Homo sapi
44	271.2	69.0	352	9	HSa556824	AJ556824 Homo sapi
45	271.2	69.0	712	9	HSRIGHVDJ	Z50007 H.sapiens l
46	271.2	69.0	819	12	HSa225092	AJ225092 Synthetic
47	271	69.0	321	9	HSa406683	AJ406683 Homo sapi
48	270.8	68.9	378	9	AF004319	AF004319 Homo sapi
49	270.6	68.9	60962	2	AC103742	AC103742 Homo sapi
50	270.4	68.8	357	9	HUWIGHV3C	L19904 Human clone
51	270.4	68.8	486	9	HSIG486	X61011 Human Immun
52	270.2	68.8	294	9	HSIGDP77	Z14073 H.sapiens g
53	270.2	68.8	336	9	HSa406723	AJ406723 Homo sapi
54	270.2	68.8	336	9	HSRIGHVD3	X99354 H.sapiens m
55	270.2	68.8	346	9	HSa556832	AJ556832 Homo sapi
56	270	68.7	1630	9	BC024289	BC024289 Homo sapi
57	269.6	68.6	378	9	HSIGVHC25	Z37313 H.sapiens r
58	269.6	68.6	393	9	HSU001171	AJ001171 Homo sapi
59	269.6	68.6	423	9	AF062121	AF062121 Homo sapi
60	269.2	68.5	378	9	HSa239390	AJ239390 Homo sapi

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

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RESULT 1
LOCUS AR160968 393 bp DNA linear PAT 17-OCT-2001
DEFINITION AR160968 Sequence 97 from patent US 6255455.
ACCESSION AR160968
VERSION AR160968.1 GI:16226171
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Siegel,D.L.
TITLE Rh(D)-binding proteins and magnetically activated cell sorting
JOURNAL Patent: US 6255455-A 97 03-JUL-2001;
FEATURES
Source Location/Qualifiers
BASE COUNT 88 a 99 c 120 g 86 t
ORIGIN

Query Match 100.0%; Score 393; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 6,7e-116;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGGTGAGTCTGGGGGAGGCTGTCAGGCTGGGGG 60
DB 1 GAGGTGCAGCTGCTCGAGTCTGGGGGTGAGTCTGGGGGAGGCTGTCAGGCTGGGGG 60
QY 61 TCCCTGAGACTCTCTCTGTCAGCCTCTGATTCACCTCTAGTAGCTATAGTCAGCTGG 120
DB 61 TCCCTGAGACTCTCTCTGTCAGCCTCTGATTCACCTCTAGTAGCTATAGTCAGCTGG 120
QY 121 GTCCGCGCAGGCTCCAGGAGGAGGGCTGAGTGGTCTCATTCATTAGTATAGTAT 180
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DB 181 TACATATCTAGCAGACGACGATGAGAGGCGGATTCACCTCCAGAGACAGCCCAAG 240
QY 181 TACATATCTAGCAGACGACGATGAGAGGCGGATTCACCTCCAGAGACAGCCCAAG 240
DB 181 TACATATCTAGCAGACGACGATGAGAGGCGGATTCACCTCCAGAGACAGCCCAAG 240
QY 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
DB 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
QY 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
DB 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
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DB 301 GCGAGAGATTCTAGATAGCAATATTCCTCGCTGGCTTGGAGAGCGATATGACGTC 360
QY 361 TGGGGCCAGGAGGACCGGCTCATCGTCTCTCA 393
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RESULT 2
LOCUS AF044446 393 bp mRNA linear SYN 31-OCT-2001
DEFINITION AF044446 Synthetic construct from Homo sapiens clone E03 anti-Rh(D) antibody
ACCESSION AF044446
VERSION AF044446.1 GI:3046463
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 393)
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
TITLE Isolation of cell surface-specific human monoclonal antibodies
JOURNAL using phage display and magnetically activated cell sorting:
MEDLINE applications in immunohematology
PUBMED J. Immunol. Methods 206 (1-2), 73-85 (1997)
JOURNAL 97469098
PUBMED 9328570

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REFERENCE 2 (bases 1 to 393)
AUTHORS Chang,T.Y. and Siegel,D.L.
TITLE Genetic and immunological properties of phage-displayed human
JOURNAL anti-Rh(D) antibodies: implications for Rh(D) epitope topology
MEDLINE Blood 91 (8), 3066-3078 (1998)
PUBMED 98200617
REFERENCE 3 (bases 1 to 393)
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
FEATURES
Source Location/Qualifiers
BASE COUNT 88 a 99 c 120 g 86 t
ORIGIN

Query Match 100.0%; Score 393; DB 12; Length 393;
Best Local Similarity 100.0%; Pred. No. 6,7e-116;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGGTGAGTCTGGGGGAGGCTGTCAGGCTGGGGG 60
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QY 61 TCCCTGAGACTCTCTCTGTCAGCCTCTGATTCACCTCTAGTAGCTATAGTCAGCTGG 120
DB 61 TCCCTGAGACTCTCTCTGTCAGCCTCTGATTCACCTCTAGTAGCTATAGTCAGCTGG 120
QY 121 GTCCGCGCAGGCTCCAGGAGGAGGGCTGAGTGGTCTCATTCATTAGTATAGTAT 180
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DB 181 TACATATCTAGCAGACGACGATGAGAGGCGGATTCACCTCCAGAGACAGCCCAAG 240
QY 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
DB 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
QY 241 AACTCAGCTATCTGCAATGAAAGCCCTGAGAGCGACAGCCGCTGTACTACTGT 300
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DB 361 TGGGGCCAGGAGGACCGGCTCATCGTCTCTCA 393

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RESULT 3
LOCUS ARI60967 381 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 96 from patent US 6255455.
ACCESSION ARI60967
VERSION ARI60967.1 GI:16226167
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 381)
AUTHORS Siegel,D.L.
TITLE Rh(D)-binding proteins and magnetically activated cell sorting
method for production thereof
JOURNAL Patent: US 6255455-A 96 03-JUL-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 87 a 98 c 113 g 83 t
ORIGIN
Query Match 92.5%; Score 363.6; DB 6; Length 381;
Best Local Similarity 98.9%; Pred. No. 2.2e-106;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCACG 83
Db 12 GCTGAGTCTGGGGAGGCGCTGTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCACG 71
QY 84 CTCTGATTACCTTACAGTACCTATAGCATGCTGCTGCGCCAGGGTCCAGGAAAGG 143
Db 72 CTCTGATTACCTTACAGTACCTATAGCATGCTGCTGCGCCAGGGTCCAGGAAAGG 131
QY 144 GCTGAGTGGGTCTCATCTCAATTAATATAGTAATACTTACATATACGAGAGCGAGT 203
Db 132 GCTGAGTGGGTCTCATCTCAATTAATATAGTAATACTTACATATACGAGAGCGAGT 191
QY 204 GAAGGGCCGATTACACATCTCCAGAGACAGCCAGAACACACTGCTATTCGCAATGAA 263
Db 192 GAAGGGCCGATTACACATCTCCAGAGACAGCCAGAACACACTGCTATTCGCAATGAA 251
QY 264 CAGCTGAGAGCCAGACAGCGCTGTACTACTGTGCGAGAGATTAGATACAGTAA 323
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QY 324 TTTCCTCCGTTGGGTTCGAGACGAGGTATGAGAGCTGTGGGCCAAGGACACGGTCAT 383
Db 312 TTTCCTCCGTTGGGTTCGAGACGAGGTATGAGAGCTGTGGGCCAAGGACACGGTCAT 371
QY 384 CGTCTCTCA 393
Db 372 CGTCTCTCA 381

RESULT 4
LOCUS AF044445 381 bp mRNA linear SYN 31-OCT-2001
DEFINITION Synthetic construct from Homo sapiens clone E01 anti-Rh(D) antibody
ACCESSION AF044445
VERSION AF044445.1 GI:3046461
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 381)
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
TITLE Slagel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
using phage display and magnetically-activated cell sorting;
applications in Immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)

MEDLINE 97469098
PUBMED 9328570
REFERENCE 2 (bases 1 to 381)
AUTHORS Chang,T.Y. and Siegel,D.L.
TITLE Genetic and immunological properties of phage-displayed human anti-Rh(D) antibodies: implications for Rh(D) epitope topology
JOURNAL Blood 91 (8), 3066-3078 (1998)
MEDLINE 98200617
PUBMED 9531621
REFERENCE 3 (bases 1 to 381)
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania, 36th & Hamilton, Philadelphia, PA 19104, USA
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
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V.segment 1..18
misc_feature /note="pcomb3H"
primer_bind 19..24 /note="VH1f/VH3f primer"
BASE COUNT 87 a 98 c 113 g 83 t
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Query Match 92.5%; Score 363.6; DB 12; Length 381;
Best Local Similarity 98.9%; Pred. No. 2.2e-106;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCACG 83
Db 12 GCTGAGTCTGGGGAGGCGCTGTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCACG 71
QY 84 CTCTGATTACCTTACAGTACCTATAGCATGCTGCTGCGCCAGGGTCCAGGAAAGG 143
Db 72 CTCTGATTACCTTACAGTACCTATAGCATGCTGCTGCGCCAGGGTCCAGGAAAGG 131
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Db 312 TTTCCTCCGTTGGGTTCGAGACGAGGTATGAGAGCTGTGGGCCAAGGACACGGTCAT 371
QY 384 CGTCTCTCA 393

Db 372 CGTCTCTCA 381

RESULT 5
LOCUS HSA234196
DEFINITION Homo sapiens mRNA for Ig heavy chain variable region, clone

6/9/10. HSA234196 435 bp DNA linear PRI 10-DEC-1999

ACCESSION AJ234196.1 GI:3821137
VERSION heavy chain; immunoglobulin superfamily; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 435)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS Noppe, S.M., Heilmann, C., Bakus, M.H., Brissinck, J., Schots, R. and Thielemans, K.

TITLE The genetic variability of the VH genes in follicular lymphoma: the impact of the hypermutation mechanism

JOURNAL 20050318
PUBMED 10583269

REFERENCE 2 (bases 1 to 435)
Noppe, S.M.

AUTHORS Direct Submission
TITLE Submitted (23-OCT-1998) Noppe, S.M., Laboratory of Physiology, Free University of Brussels, Laarbeeklaan 103/E, 1090 Brussels, BELGIUM

FEATURES
SOURCE Location/Qualifiers

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/isolate="follicular lymphoma patient"

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BASE COUNT 93 a 104 c 135 g 103 t

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Query Match 77.9%; Score 306; DB 9; Length 435;
Best Local Similarity 91.1%; Pred. No. 1e-87; Mismatches 30; Indels 3; Gaps 1;

Matches 337; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

24 GGTGAGCTCTGGGAGGCTGGTCAAGCCCTGGGGGGTCCCTGAGACTCTCTCTGCAC 83

69 GGTGAGCTCTGGGAGGCTGGTCAAGCCCTGGGGGGTCCCTGAGACTCTCTCTGCAC 128

84 CTCTGAGTTCACTTCACTAGCTATAGCACTGGGCTCCGCGAGGCTCCAGGAAAGG 143

129 CTCTGAGTTCACTTCACTAGCTATAGCACTGGGCTCCGCGAGGCTCCAGGAAAGG 188

144 GCTGAGTGGTCTCATCTAATAGTAACTACTATACCTATACAGCAGCAGT 203

189 GCTGAGTGGTCTCATCTAATAGTAACTACTATACCTATACAGCAGCAGT 248

204 GAAGGCGCATTCACATCTCCAGAGCAACGCCAAGAACACATCTATCTCAATGAA 263

249 GAAGGCGCATTCACATCTCCAGAGCAACGCCAAGAACACATCTATCTCAATGAA 308

264 CAGCTGAGAGCCGAGCAGCGCTGTGTACTACTGCGGAGATTCATAGACAGTAA 323

309 CAGCTGAGAGCCGAGCAGCGCTGTGTGTATTACTGTGCGAGATGATAG--CACTGG 365

324 TTTCCTCGCTGGGTGGAGCAGCGATGAGAGCTGCGGCGCAAGGACCAAGCAT 383

Db 366 CTGTACCCCTCCTTAGCGTTAGCCGATAGACGCTGTGGGCGCAAGGACCAAGGTCAC 425

384 CGTCTCTCA 393

426 CGTCTCTCA 435

RESULT 6
LOCUS HSA519295
DEFINITION Homo sapiens partial mRNA for IgM immunoglobulin heavy chain

variable region (IGHV gene), clone ANBPM229. HSA519295 396 bp mRNA linear PRI 14-JAN-2003

ACCESSION AJ519295.1 GI:27753290
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 396)
Lausen, B.F., Hougs, L., Schejbel, L., Heilmann, C. and Barington, T.

AUTHORS Human memory B cells transferred by allogeneic bone marrow transplantation contribute significantly to the antibody repertoire, but fail to re-enter the process of somatic mutation upon antigenic stimulation

Unpublished
JOURNAL 2 (bases 1 to 396)
Lausen, B.F., Hougs, L., Schejbel, L., Heilmann, C. and Barington, T.

AUTHORS Direct Submission
TITLE Submitted (22-NOV-2002) Paediatric Clinic II, section 4064, Juliane Marie Centre, University Hospital Rigshospitalet, Blegdamsvej 9, Copenhagen DK-2100, Denmark

FEATURES
SOURCE Location/Qualifiers

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/db_xref="taxon:9606"

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/db_xref="GI:27753291"

/translation="GTCCEVQLVESGGLVKKPGSRLTSCAAGTFSSYNNWYROA
PCKGLMWSISSSSXYIYADSKRPTISRDNAKNSLYLQNSLRADDAVYYCAR
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1. 12

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13. 375

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13. 307

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/note="germline gene: VH3-21"

308. 312

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313. 337

/gene="IGHV"

/note="germline gene: D3-10"

338. 341

/gene="IGHV"

342. 396

/gene="IGHV"

/note="germline gene: JH6b1"

BASE COUNT 86 a 97 c 122 g 91 t

ORIGIN

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mat_peptide
V_region
V_segment
N_region
D_segment
N_region
J_segment
BASE COUNT

Query Match	75.4%;	Score 296.2;	DB 9;	Length 396;
Best Local Similarity	89.0%;	Pred. No. 1,5e-84;		
Matches 332:	Conservative	0;	Mismatches 38;	Indels 3; Gaps 1.
OY	24	GGTGGAGTCTGSGGGAGGCCTGGTCMAACCCTGGGGGGTCCTGAGACATCTCCTGTGCAGC	83	
Db	24	GGTGAGACTGTGGGGAGSCTGTGTCAACCTGTGGGGGGTCCCTGAGACATCTCCTGTGCAGC	83	
OY	84	CTCTGGAATTACCTTTCACTTAGCTATAGCATGTGCATCGGGTCCGCCAGGGTCCAGGSAAAGG	143	
Db	84	CTCTGGAATTACCTTTCACTTAGCTATAGCATGTGCATCGGGTCCGCCAGGGTCCAGGSAAAGG	143	
OY	144	GCTGGAGTGGGTCATCATTCATTAGTAATAAGTAATCTTACAATATATCTACGACAGACAGCAGT	203	
Db	144	GCTGGAGTGGGTCATCATTCATTAGTAATAAGTAATCTTACAATATATCTACGACAGACAGCAGT	203	
OY	204	GAAGGGCCGATTCACCATCTCCAGAGACACAGCCACAGAATCTGTATCTGCACAAATGAA	263	
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OY	264	CAGCCTGAGACCCGACACAGCGCTGTACTACTGTCGAGAGATTTCTAGATACAGTAA	323	
Db	264	CAGCCTGAGACCCGACACAGCGCTGTACTACTGTCGAGAGATTTCTAGATACAGTAA	323	
OY	324	TTCCT -- CTCCGTTGGGTTTGGAGCGAGCATGTGGACCTGTGGGGCCCAAGGAGACCCAGCT	380	
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OY	381	CATGCTTCCTCA 393		
Db	384	CACGCTCTCTCA 396		

RESULT 7	
AB066972	
LOCUS	AB066972 378 bp mRNA linear PRI 02-JUL-2007
DEFINITION	Homo sapiens IGH mRNA for Immunoglobulin heavy chain VHDJ region, partial cds, clone:aims0006h.
ACCESSION	AB066972
VERSION	AB066972.1 GI:21670000
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,U., Miura,K. and Kurosawa,Y. Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
TITLE	Unpublished
JOURNAL	2 (bases 1 to 378) Kurosawa,Y.
REFERENCE	Direct Submission
AUTHORS	Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-Chou, Toyooka, Aichi 470-1192, Japan (E-mail:kurosawafujita-hu.ac.jp, Tel:81-562-93-9387)
TITLE	Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/ .
JOURNAL	Location/Qualifiers
COMMENT	1. .378
FEATURES	/organism="Homo sapiens" source
SOURCE	/mol_type="mRNA" /db_xref="taxon:9606" /clone="aims0006h" /clone_1id="AIMS4" /note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow" 1. .378 /gene="IGH"
gene	

CDS	BASE COUNT	ORIGIN
<1..>378 /gene="IGH" /codon_start=1 /product="immunoglobulin heavy chain VHD region" /protein_id="BAC02010.1" /db_xref="GI:21670001" /translation="EVQLVESGGGLVPRGSLRLSCAASGFTFSYSMNWVQAQPGK LEWVSISSSSSYIYADVSKGRFTISDNKNSLYLQMSLRAEDTAVYYCARERKK VVRGKNGYGGMDVWGQGTFTVYSS"	88 a 89 c 123 g 78 t	

Query Match	Similarity	74.8%	Score 294	DB 9	Length 378
Best Local	Similarity	89.6%	Pred. No. 7	9e-84	
Matches	328	Conservative	0	Mismatches	35
				Indels	3
				Gaps	1
QY	24	GGTGAGCTCTGGGGGAGCGCTGGTCAGCCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC	83		
Db	12	GGTGAGCTCTGGGGGAGCGCTGGTCAGCCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC	71		
QY	84	CTTGTGATTCACCTTCAGTACGTATAGCATGCTGGTCCGCCAGGGTCCAGGGAGGG	143		
Db	72	CTGTGATTCACCTTCAGTACGTATAGCATGAGTGAAGTGGGTCCGCCAGGGTCCAGGGAGGG	131		
QY	144	GCTGGAGTGGGCTCATTCATTAGTAAGTAATCTCAATATCTACTACGAGACGACGT	203		
Db	132	GCTGGAGTGGGCTCATTCATTAGTAAGTAAGTAATCTCAATATCTACTACGAGACGT	191		
QY	204	GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACTCATCTGTATCTGCAATGAA	263		
Db	192	GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACTCATCTGTATCTGCAATGAA	251		
QY	264	CAGCTGAGAGCCGAGACACAGCGCTGTGTACTACTGTGCGAGAGATTCTAGATACATGA	323		
Db	252	CAGCTGAGAGCCGAGAGACAGCGCTGTGTACTACTGTGCGAGAGATTCTAGATACATGA	311		
QY	324	TTTCTCCGTTGGTGTGGGAGGAGCGTATGGAGCTCTGGGGGCCAAGGGACACGCGTAC	383		
Db	312	TTCGGGCAATTAAG--GCTACTACGATATGACCTCTGGGGGCCAAGGGACACGCGTAC	368		
QY	384	CGTCTC 389			
Db	369	CGTCTC 374			
RESULT 8	AF062202	435 bp	mRNA	linear	PRI 08-MAY-2001
LOCUS	AF062202				
DEFINITION	Homo sapiens clone 48u-42 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.				
ACCESSION	AF062202				
VERSION	AF062202.1	GI:3170866			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 435)				
TITLE	Wang, X. and Stollner, B.D.				
JOURNAL	Immunoglobulin VH gene expression in human aging				
MEDLINE	Clin. Immunol. 93 (2), 132-142 (1999)				
PUBMED	99459189				
REFERENCE	10527689				
AUTHORS	2 (bases 1 to 435)				
TITLE	Wang, X. and Stollner, B.D.				
JOURNAL	Direct Submission				
FEATURES	Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA				
SOURCE	Location/Qualifiers				
	1..435				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				

BASE COUNT 93 a 127 c 128 g 90 t
ORIGIN CYYTGMDVWGCGTTTIVSSASTKGPVFPPLAPSSKSTSGTAA"

Query Match 72.5%; Score 284.8; DB 9; Length 438;
Best Local Similarity 88.3%; Pred. No. 7.7e-81;
Matches 323; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

34 GGGGAGGCGCTGTAAAGCTGGGGGTCCTGAGACACTCTGTGACGCTGTGGATTC 93
1 GGGGAGGCGCTGTAAAGCTGGGGGTCCTGAGACACTCTGTGACGCTGTGGATTC 60
94 ACCTTCAGTACGATAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 153
61 ACCTTCAGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
154 GCTCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
121 GCTCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
214 TTCACATCTCCAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 273
181 TTCACATCTCCAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 240
274 GCGGAGCAGCAGCGCTGTACTACTGTGCGAGAGAT-----TCTAGATACAGTATTC 327
241 GCGGAGCAGCAGCGCTGTACTACTGTGCGAGAGAT-----TCTAGATACAGTATTC 300
328 CTCCTGTGGGTTGGAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 387
301 GTTACTGTGCTACTACCTACCGGATGATGATGATGATGATGATGATGATGATGAT 360
388 TCCTCA 393
361 TCCTCA 366

RESULT 14 372 bp DNA linear PRI 02-MAY-2001
AF170095
LOCUS Homo sapiens isolate MCL-BV/128 immunoglobulin heavy chain VDJ
DEFINITION region (IGH) gene, IGH-F allele, partial cds.
ACCESSION AF170095.1 GI:5917697
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 372)
Laszlo, T., Nagy, M., Kelenyi, G. and Matolcsy, A.
Immunoglobulin V(H) gene mutational analysis suggests that blastoid
variant of mantle cell lymphoma derives from different stages of
B-cell maturation
Leuk. Res. 24 (1), 27-31 (2000)
20098130
10634642
2 (bases 1 to 372)
Matolcsy, A.
Direct Submission
Submitted (21-JUL-1999) Department of Pathology, University Medical
School of Pecs, Szigeti ut 12, Pecs, Baranya 7624, Hungary
FEATURES
Source
1..372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="MCL-BV/128"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32"
/cell_type="B-cell"
/tissue_type="mantle cell blastic variant of non-Hodgkin's
lymphoma"

BASE COUNT 89 a 93 c 111 g 79 t
ORIGIN

Query Match 72.3%; Score 284; DB 9; Length 372;
Best Local Similarity 87.6%; Pred. No. 1.4e-80;
Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

24 GGTGAGTGTGGGGAGGCGCTGTCAAGCGTGGGGGTCCTGAGACTCTGTGACAC 83
9 GGTGAGTGTGGGGAGGCGCTGTCAAGCGTGGGGGTCCTGAGACTCTGTGACAC 68
84 CTCGTGATTCACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 143
69 CTCGTGATTCACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 128
144 GCTGAGTGTGGTCTCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 203
129 GCTGAGTGTGGTCTCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 188
204 GAAGGCGCATTCACCATCTCCAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCA 263
189 GAAGGCGCATTCACCATCTCCAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCA 248
264 CAGCCTGAGAGCGGAGCAGCGCTGTGATGATGATGATGATGATGATGATGATGAT 323
249 CAGCCTGAGAGCGGAGCAGCGCTGTGATGATGATGATGATGATGATGATGATGAT 305
324 TTTCCTCCGTTGGTGGAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 383
306 ---CAGCTGGAGCGATFACTACTACTGACGCTGTGGGCAAGGACCAAGCGTGTAC 362
384 CGTCTCCTCA 393
363 CGTCTCCTCA 372

RESULT 15 387 bp mRNA linear PRI 15-APR-2003
HSAS55251
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable
DEFINITION region (IGHV gene), isolate B-CLL G002.
ACCESSION AJ555251.1 GI:29892968
VERSION
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Fais, F., Morabito, F., Stelitano, C., Callea, V., Zanardi, S.,
Scudiletta, M., Varese, P., Ciccone, E. and Grossi, C.
CD1d on B-chronic lymphocytic leukemia cells mediates
a-galactosylceramide presentation to natural killer T lymphocytes
Unpublished
2 (bases 1 to 387)
Fais, F.
Direct Submission

JOURNAL
Submitted (03-APR-2003) Fais F., Department of Experimental
medicine, Human Anatomy Section, Via De Toni 14, 16132, Genova
ITALY

FEATURES	Location/Qualifiers
source	1. .387

BASE COUNT	87 a	98 c	116 g	86 t
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Query Match	72.0%	Score 283;	DB 9;	Length 387;
Best Local Similarity	88.5%	Pred. No. 2.9e-80;		
Matches 330: Conservative	0:	Mismatches 40:	Indels 3:	Gaps 2

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Db	12	GGTGGAGTCGTGGGGGAGGCGCTGTCACAGCCGCGGGGGGTCCCTGAGACTCCGTCAC	71
QY	84	CTCTGGATTCAACCTTCAGTACCTPAPAGCATGACATGGTGTCCGCGCAGAGTCGAGGAAGG	143
Db	72	CTCTGGATTCAACCTTCAGTACCTPAPAGCATGAGACTGGTGTCCGCGCAGAGTCGAGGAAGG	131
QY	144	GCTGGAGTGGGGTCTATCTCATTAGTAATAGTAATACTTAACTATCTATAGCAGACGAT	203
Db	132	GCTGGAGTGGGGTCTATCTCATTAGTAATAGTAATAGTAATAGTAATCTATCTATAGCAGACGAT	191
QY	204	GAAGGGCCGATTACACATCTCCACAGACCAAGCCAGAAATCACTGTATCTGCAATGAA	263
Db	192	GAAGGGCCGATTACACATCTCCACAGACCAAGCCAGAAATCACTGTATCTGCAATGAA	251
QY	264	CAGCTGAGAGCCGACAGCACAGGCTGTGTACTACTGTGGAGGAAATCTTA--GATACAGT	321
Db	252	CAGCTGAGAGCCGACAGCACAGGCTGTGTATTTACTGTGCGAGAGCCCTCCAAATATGTATAT	311
QY	322	AATTTTCCTCCGTTGGGTGCG--AGCGAGGCTATGAGACGTCGTGGGGCCAAAGGACACGCT	380
Db	312	ACTTACACAGCTGCTATCTACGGCTGTGGACTACTTTGACTACTGTGGGGGCCAAGGAACCTGTG	371
QY	381	CATGCTGTCTCTCA 393	
Db	372	CACGCTGTCTCTCA 384	

RESULT 16	AF174081	375 bp	MRNA	linear	PRT 08-MAY-2001
LOCUS	AF174081				
DEFINITION	Homo sapiens clone sc48u-100 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.				
ACCESSION	AF174081				
VERSION	AF174081.1	GI:5834121			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Wang, X. and Stollari, B. D.				
TITLE	Immunoglobulin VH gene expression in human aging				

JOURNAL	Clín. Immunol. 93 (2), 132-142 (1999)
MEDLINE	99459182
PUBMED	10527689
REFERENCE	2 (pages 1 to 375)
AUTHORS	Wang, X. and Stollár, B.D.
TITLE	Direct Submersion
JOURNAL	Submitted (02-AUG-1999) Biochemistry Department, Tufts University
FEATURES	School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
Source	Location/Qualifiers 1..375

BASE COUNT	85 a	90 c	117 g	.83 t
ORIGIN				
Query Match	71.1%	Score 279.6;	DB 9;	Length 375;
Best local Similarity	87.0%;	Pred. No. 3.7e-79;		
Matches 322; Conservative	0;	Mismatches 39;	Indels 9;	Gaps 1;

QY	24	AGTGGAGTCTGGGGGAGGCGTGGTCAACCCCTGGGGGGTCCCTGGAGCTCTCTGTCAGC	83
Db	12	GGTGGAGTCTGGGGGAGGCTTGGTCAACGCTGGGGGGTCCCTGGAGCTCTCTGTGCAGC	71
QY	84	CTCTGGATTACACCTTCAGTACGCTATAGCATCTACTGGGTCCGCGAGGCTCAGGGAAAGG	143
Db	72	CTCTGGATTACACCTTCAGTACGCTATAGCATTAACCTGGGTCCGCGAGGCTCAGGGAAAGG	131
QY	144	GCTGGAGTGGGCTCATCTGATTAAGTAATGTAATTAATTAATACATACGCAAGCAGT	203
Db	132	GCTGGAGTGGGTTTATATACATTAGTAGTAGTAGTAGTAGTACATATACATACGCAAGCTGT	191
QY	204	GAAGGGCCGATTCACCATCTCCAGAGAACACGCCAAGATCTACTGTATATGCAATGAA	263
Db	192	GAAGGGCCGATTCACCATCTCCAGAGAACATGCCAAGATCTACTGTATATGCAAAATGAA	251
QY	264	CAGCCTGAGAGCCGAGGACACAGCGGTGTACTACTGTGCGAGAGATCTTGATATACAGTAA	323
Db	252	CAGCCTGAGAGCCGAGGACACAGCGGTGTATTTACTGTGCGAGAGATTTGGAGCTGTGCGCA	311
QY	324	TTTCTCCGCTTGGTTCGAGACGACCGATATGAGAGCTCTGGGGCCAAAGGACACCGCTCAT	383
Db	312	GTATACACTACT-----ACTAGGTATATGAGCTCTGGGGCCAAAGGACACCGCTCAT	362
QY	384	CGTCTGCTCA	393
Db	363	CGTGTGCTCA	372

RESULT	17
HSY12442	
LOCUS	389 bp DNA linear PRI 15-JAN-1996
DEFINITION	H.sapiens Igh gene, partial, isolate Lymphoma 222.
ACCESSION	V12442
VERSION	V12442.1 GI:20734423
KEYWORDS	CDR3 region; constant region; heavy chain; immunoglobulin. Homo sapiens (human)
SOURCE	

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS van Belzen, N., Hupkes, P.E., Doekharan, D., Hoogeveen-Westerveld, M.,
Dossers, L.C., and van 't Veer, M.B.
TITLE Detection of minimal disease using rearranged immunoglobulin heavy
chain genes from intermediate- and high-grade malignant B cell
non-Hodgkins lymphoma
JOURNAL Leukemia 11 (10), 1742-1752 (1997)
MEDLINE 97464475
PUBMED 9324296
REFERENCE 2 (bases 1 to 389)
AUTHORS Van Belzen, N.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1997) N. Van Belzen, Erasmus University
Rotterdam, Department of Hematology, PO Box 1738, 3000 DR
Rotterdam, NETHERLANDS

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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/rearranged
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EWSSISSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRADFTAYVYCARREVEV
PIFRNIOGSAFDIWGGQIVTVSSG"
296..339
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/note="CDR3 domain"

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BASE COUNT 94 a 93 c 116 g 86 t
ORIGIN

Query Match 70.9%; Score 278.8; DB 9; Length 389;
Best Local Similarity 85.9%; Pred. No. 6.7e-79;
Matches 323; Conservative 0; Mismatches 47; Indels 6; Gaps 1:

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QY 24 GGTGAGTCTGGGGGAGGCTGTGTAACGCTGGGGGTCCTCGAAGCTCTCTGTGCAGC 83
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DB 11 GGTGAGTCTGGGGGAGGCTGTGTAACGCTGGGGGTCCTCGAAGCTCTCTGTGCAGC 70
QY 84 CTCGTGATTCACCTTCAGTATAGCATGATGCACTGGGTCGCCAGGGTCAGGGAAGG 143
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 71 CTCGTGATTCACCTTCAGTATAGCATGATGCACTGGGTCGCCAGGGTCAGGGAAGG 130
QY 144 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATCTTACATATACAGAGCAGT 203
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 131 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATCTTACATATACAGAGCAGT 190
QY 204 GAAGGCGGATTCACCATCTCCAGAGACAGCCCAAGAACTACTGTCATCAATGAA 263
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DB 191 GAAGGCGGATTCACCATCTCCAGAGACAGCCCAAGAACTACTGTCATCAATGAA 250
QY 264 CAGCTGAGAGCCGAGACAGCGGTGTACTACTGTGCGAGAGATCTAGATA----- 317
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 251 CAGCTGAGAGCCGAGACAGCGGTGTACTACTGTGCGAGAGATCTAGATA----- 310
QY 318 CAGTAATTTCTCCGTTGGGTTCCGAGCGAGCGTATGAGACGTCTGGGGCCAAGGACAC 377
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 311 TACATTTTAAACATCAATCGGGGATGCTTTGATATCTGGGGCCAAGGACAAAT 370
QY 378 GGTGATGCTGTCCTCA 393
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 371 GGTGATGCTGTCCTCA 386
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RESULT 18
AF466106 384 bp DNA linear PRI 18-SEP-2002
LOCUS partial cds.
DEFINITION Homo sapiens immunoglobulin heavy chain variable region gene.
ACCESSION AF466106
VERSION AF466106.1 GI:18496730
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 384)
AUTHORS Zhu, D., Orchard, J., Oscier, D.G., Wright, D.H. and Stevenson, F.K.
TITLE V(H) gene analysis of splenic marginal zone lymphomas reveals
diversity in mutational status and initiation of somatic mutation
in vivo
JOURNAL Blood 100 (7), 2659-2661 (2002)
MEDLINE 22224400
PUBMED 12239182
REFERENCE 2 (bases 1 to 384)
AUTHORS Zhu, D., Orchard, J., Oscier, D.G., Wright, D.H. and Stevenson, F.K.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2002) Molecular Immunology Group, Tenovus
Laboratory, Cancer Sciences Division, University of Southampton,
Tremora Road, Southampton SO16 6YD, UK
Ig VH sequence from SMZL case ME.

COMMENT
FEATURES
source location/Qualifiers
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CDS
BASE COUNT 85 a 96 c 115 g 88 t
ORIGIN

Query Match 70.9%; Score 278.6; DB 9; Length 384;
Best Local Similarity 86.1%; Pred. No. 7.7e-79;
Matches 321; Conservative 0; Mismatches 49; Indels 3; Gaps 1:

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QY 24 GGTGAGTCTGGGGGAGGCTGTGTAACGCTGGGGGTCCTCGAAGCTCTCTGTGCAGC 83
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 12 GGTGAGTCTGGGGGAGGCTGTGTAACGCTGGGGGTCCTCGAAGCTCTCTGTGCAGC 71
QY 84 CTCGTGATTCACCTTCAGTATAGCATGATGCACTGGGTCGCCAGGGTCAGGGAAGG 143
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DB 72 CTCGTGATTCACCTTCAGTATAGCATGATGCACTGGGTCGCCAGGGTCAGGGAAGG 131
QY 144 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATCTTACATATACAGAGCAGT 203
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DB 132 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATCTTACATATACAGAGCAGT 191
QY 204 GAAGGCGGATTCACCATCTCCAGAGACAGCCCAAGAACTACTGTCATCAATGAA 263
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 192 GAAGGCGGATTCACCATCTCCAGAGACAGCCCAAGAACTACTGTCATCAATGAA 251
QY 264 CAGCTGAGAGCCGAGACAGCGGTGTACTACTGTGCGAGAGATCTAGATA----- 323
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 252 CCGCTGAGAGCCGAGACAGCGGTGTACTACTGTGCGAGAGATCTAGATA----- 311
QY 324 TTTCCTCGTTGGGTTCCGAGCG--ACGATGAGACGTCTGGGGCCAAGGACCAAGGT 380
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Db	312	ACGTTTGGGGAGATTATCGTGGCTACTACTTGTACTACTGGGCGAGGGAACCTGTG	37
QY	381	CATGCTCTCTCA 393	
Db	372	CACGCTCTCTCA 384	
RESULT 19			
AF466107			
LOCUS			
DEFINITION			
AF466107			
VERSION			
KEYWORDS			
AF466107.1			
GI:18496732			
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384 bp			
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linear			
PRI 18-SEP-2002			
partial cds.			
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AF466107.1			
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AF466107			
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linear			
PRI 18-SEP-2002			
partial cds.			
AF466107			
AF466107.1			
GI:18496732			
AF466107			
384 bp			
DNA			
linear			
PRI 18-SEP-2002			
partial cds.			
AF466107			
AF466107.1			
GI:18496732			
AF466107			
384 bp			
DNA			
linear			
PRI 18-SEP-2002			
partial cds.			
AF466107			
AF466107.1			
GI:18496732			
AF466107			
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linear			
PRI 18-SEP-2002			
partial cds.			
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AF466107.1			
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linear			
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partial cds.			
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AF466107.1			
GI:18496732			
AF466107			
384 bp			
DNA			
linear			
PRI 18-SEP-2002			
partial cds.			
AF466107			
AF466107.1			
GI:18496732			
AF466107			
384 bp			
DNA			
linear			
PRI 18-SEP-2002			
partial cds.			
AF466107			
AF466107.1			
GI:18496732			
AF466107			
38			

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Db	252	CCGCTGTAGAGCCGAGAGCAGACGGCTGTGTATTACTGTGCGAGAGATTCTAAGGCCACAT	311
OY	324	TTTCTCTCGTTGGGTGGAGAGC---ACGATATGAGCTGTGGGCGCAAGGACCAAGCT	380
Db	312	ACGTTTGGGGAGATTATATGCTGTGCTACTACTTTTACTACTGTGGCCAGGAAACCTGT	371
OY	381	CATGCTCTCTCTCA	393
Db	372	CACGCTCTCTCTCA	384
RESULT 20			
HSR0221			
LOCUS	HSR0221	441 bp	mRNA
DEFINITION	H.sapiens rearranged VDJ region (R0221).	linear	PRI 29-FEB-1996
ACCESSION	X81751		
VERSION	X81751.1	GI:1209423	
KEYWORDS	diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Metazoa; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1		
TITLE	Milli,M., Schiff,C., Fougereau,M. and Tonnelle,C. The VDJ repertoire expressed in human preB cells reflects the selection of bone fide heavy chains		
JOURNAL	Eur. J. Immunol. 26.(1), 63-69 (1996)		
MEDLINE	96152725		
PUBMED	8566085		
REFERENCE	2 (bases 1 to 441)		
AUTHORS	Tonnelle,C.		
TITLE	Direct Submision		
JOURNAL	Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie		
COMMENT	Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie		
FEATURES	Marseille-Umuniy, Case 906, 13288 Marseille, Cedex 9, FRANCE		
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	/tissue_type="bone marrow"		
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	/rearranged		
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V-region	/product="immunoglobulin heavy chain V region"		
	354..389		
D-segment	/product="immunoglobulin heavy chain D segment"		
	390..441		
J-segment	/product="immunoglobulin heavy chain J segment"		
	98 a 94 c 134 g 115 t		
BASE COUNT	70.9%: Score 278.6; DB 9; Length 441;		
ORIGIN	Best local similarity 86.1%; Pred. No. 7.9e-79;		
Query Match	Matches 321; Conservative 0; Mismatches 49; Indels 3; Gaps 1;		
OY	24	GGTGGAGCTTCGGGAGAGCGCTGTGTCACAGCCGTGGGGGCTCTGAGACTTCCTGTGCAGC	83
Db	69	GGTGGAGCTTCGGGAGAGCGCTGTGTACACACCTGGAGGGTCCCTGAGACTTCCTGTGCAGC	128
OY	84	CTCTTGATTCACCTTCAGTACGCTTATGACGACACTGGGTCCGCCAGGAGTCAGGAAAGG	143
Db	129	CTCTGGATTCACCTTCAGTACGCTTATGAAAGTAACTGGGTCCGCCAGGAGTCAGGAAAGG	188
OY	144	GCTGGAGTGGGTCTCATCATTCATTAGTAATAGTAATACCTTACATATACGACGACGAGCT	203

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Db      189  GCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTACCATATATACTACGACACTGTGT 248
OY      204  GAAGGGCCGATTTCACCATCTCCAGAGACACGCCAAGAATCCTGTATCTGCAATGAA 263
        |||||
Db      249  GAAGGGCCGATTTCACCATCTCCAGAGACACGCCAAGAATCTGTATCTGCAATGAA 308
        |||||
OY      264  CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
        |||||
Db      309  CAGCCTGAGAGCCGAGACACGCGTGTATTACTGTGCGAGAGACCGGAAGTATTACGA 368
        |||||
OY      324  TTTCCTCCGTTGGTTCCGA---GCGAGGTTATGACGTCCTGGGCCAAGGACCAACGCT 380
        |||  |||  |
Db      369  TTTTGGAGTGGTTATTATCTACTACGATATGACGCTGGGGCCAAAGGACCAACGCT 428
        |||  |||  |
OY      381  CATCGTCTCTCA 393
        |||||
Db      429  CACCGTCTCTCA 441
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Search completed: September 24, 2003, 04:04:36
Job time : 2212 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2003, 22:34:02 ; Search time 269 Seconds
(without alignments)
3943.789 Million cell updates/sec

Title: US-09-848-798a-97

Perfect score: 393
Sequence: 1 gaggtgcagctgcctcagtc.....ccacgycatcgtctcctca 393

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	393	100.0	393	22	AAH68642	Human anti-Rh(D) c
2	363.6	92.5	381	22	AAH68641	Human anti-Rh(D) c
3	272.2	69.3	311	23	ABS46318	Human liver single
4	272.2	69.3	311	24	ABS20923	Human genome-deriv
5	272.2	69.3	519	16	AA078959	Human immunoglobul
6	271.8	69.2	375	22	AAF29047	Human HIV-1 monocl
7	269.6	68.6	348	24	AAD46290	Human KDR (VEGFR-2
8	269.6	68.6	348	24	AAD46292	Human KDR (VEGFR-2

9	269.6	68.6	348	25	ABT23325	VEGF binding relat
10	269.6	68.6	348	25	ABT23327	VEGF binding relat
11	268.8	68.4	376	24	ABS62722	Anti-IGF-IR antibo
12	268	68.2	348	24	AAD46294	Human KDR (VEGFR-2
13	268	68.2	348	25	ABT23329	VEGF binding relat
14	268	68.2	458	22	AAH41153	Human coding sequ
15	261.6	66.6	376	24	ABS62704	Anti-IGF-IR antibo
16	261.2	66.5	381	20	AAK77236	Human DA.5 heavy c
17	261.2	66.5	414	19	NAIV68537	Nucleotide sequenc
18	260.6	66.3	519	20	AAZ20407	IGG antibody 2.1.1
19	260.2	66.2	1630	21	AAZ50587	HD70scfV-CH1-GM-CS
20	260.2	66.2	1630	21	AAZ50588	HD70scfV-CK-Interl
21	260	66.2	816	24	ABK43226	DNA encoding anti
22	259.2	66.0	1413	21	AAK43935	DNA encoding the h
23	258.8	65.9	381	22	AAK3516	DNA encoding anti-
24	257.8	65.6	743	16	AA078986	Human immunoglobul
25	255	64.9	376	18	AAIT3529	DNA encoding anti-
26	253.6	64.5	406	15	AA06539	Variable heavy cha
27	253.2	64.4	429	21	AAAL3935	Human p19p monocl
28	252.8	64.3	437	24	ABL33509	Human recombinant
29	252	64.1	375	24	ABS62700	Anti-IGF-IR antibo
30	252	64.1	562	21	AAK46886	DNA encoding the h
31	251.6	64.0	429	21	AAAL3939	Human p19p monocl
32	251	63.9	762	19	AAV49460	cDNA encoding huma
33	250.6	63.8	357	22	AAH47732	Nucleotide sequenc
34	250.4	63.7	474	25	ABZ22308	S. pneumoniae pps-
35	250.4	63.7	520	25	ABT31879	Anti-CD40 monoclon
36	250	63.6	429	21	AAAL3936	Human p19p monocl
37	249	63.4	354	22	AAK39470	Human p19p monocl
38	248.8	63.3	375	25	AAK24184	Anti-Egfr antibody
39	248.8	63.3	456	11	AAK03610	Sequence encoding
40	248.4	63.2	429	21	AAAL3930	Human p19p monocl
41	248.4	63.2	429	21	AAAL3931	Human p19p monocl
42	248.4	63.2	429	21	AAAL3932	Human p19p monocl
43	248.4	63.2	429	21	AAAL3933	Human p19p monocl
44	248.4	63.2	429	21	AAAL3937	Human p19p monocl
45	248.4	63.2	1458	22	AAAS2625	Human cDNA encodin
46	247.6	63.0	527	24	ABL65878	Lung cancer relate
47	247.6	63.0	527	24	ABL65879	Thyroid cancer rel
48	247.2	62.9	375	11	AAK03608	Sequence encoding
49	246.8	62.8	354	21	AAK69948	Human anti-HBS ant
50	246.8	62.8	393	22	AAH47730	Nucleotide sequenc
51	246.8	62.8	718	24	ABS62724	Anti-IGF-IR antibo
52	245.8	62.5	715	16	AA078949	Human immunoglobul
53	245.6	62.5	437	24	ABL53510	Human recombinant
54	245.6	62.5	437	24	ABL53511	Human recombinant
55	245.6	62.5	4026	24	ABK81191	DNA encoding immun
56	245.4	62.4	1605	22	AAH18432	Human cDNA sequenc
57	245	62.3	296	24	ABS62711	Germline anti-IGF-
58	245	62.3	349	22	AAK3504	DNA encoding anti-
59	244.8	62.3	437	24	ABL53508	Human recombinant
60	244.4	62.2	372	20	AAV72230	Human anti-GP11b/I

ALIGNMENTS

RESULT 1
AAH68642
ID AAH68642 standard; DNA: 393 BP.
AC AAH68642;
XX
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) chain E03 nucleotide sequence.
XX
KW Human: anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
OS Homo sapiens.
XX
XX US6255455-B1.

XX 03-JUL-2001.
PD
XX
PF 29-JAN-1999; 990S-0240274.
XX
PR 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX WPI: 2001-388931/41.
XX P-PSDB; AAG93585.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 2; Column 53; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG93558 to AAG93669 represent the nucleotide sequence which encode
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
XX Sequence 393 BP; 88 A; 99 C; 120 G; 86 T; 0 other;

Query Match 100.0%; Score 393; DB 22; Length 393;
Best Local Similarity 100.0%; Pred. No. 4.4e-107;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTGCAAGCTGCTGAGTGTGGGTGAGTGTGGGAGGAGGCTGTCAGACCTCGGGGGG 60
DB 1 GAGGTGCAAGCTGCTGAGTGTGGGTGAGTGTGGGAGGAGGCTGTCAGACCTCGGGGGG 60
QY 61 TCCCTGAGACCTCTCTGTCAGAGCCCTGTCAGTTCACCTTCACTAGCTATAGCATGCACTGG 120
DB 61 TCCCTGAGACCTCTCTGTCAGAGCCCTGTCAGTTCACCTTCACTAGCTATAGCATGCACTGG 120
QY 121 GTCCGCCAAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 GTCCGCCAAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 TACATATCTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 240
DB 181 TACATATCTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 240
QY 241 AACCTACTGTATCTGCAATATGAACAGCTTGAGAGCCGACGACGACGACGACGACGACGACGAC 300
DB 241 AACCTACTGTATCTGCAATATGAACAGCTTGAGAGCCGACGACGACGACGACGACGACGACGAC 300
QY 301 GCGAGAGATTTTGTATATAGTAATTTCTCCGTTGGGTTGCGAGCAGCAGTATGAGACGTC 360
DB 301 GCGAGAGATTTTGTATATAGTAATTTCTCCGTTGGGTTGCGAGCAGCAGTATGAGACGTC 360
QY 361 TGGGGCCAAAGGACGACGATCATGTCCTCA 393
DB 361 TGGGGCCAAAGGACGACGATCATGTCCTCA 393
RESULT 2
AAH68641
ID AAH68641 standard; DNA; 381 BP.
XX

AC AAH68641;
XX 14-SEP-2001 (first entry)
XX Human anti-Rh(D) chain E011s nucleotide sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 990S-0240274.
XX
XX 11-OCT-1996; 96US-0028550.
XX 10-APR-1998; 98US-0081380.
XX 27-JUN-1997; 97US-0884045.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX WPI: 2001-388931/41.
XX P-PSDB; AAG93584.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 2; Column 53; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG93558 to AAG93669 represent the nucleotide sequence which encode
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
XX Sequence 381 BP; 87 A; 98 C; 113 G; 83 T; 0 other;
SO
Query Match 92.5%; Score 363.6; DB 22; Length 381;
Best Local Similarity 98.9%; Pred. No. 2.5e-98;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 24 GGTGAGATCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 83
DB 12 GGTGAGATCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 71
QY 84 CTCTGATTCACCTTCACTAGTATAGCATGACACTGAGGTCGCCAGAGGTCAGGAGAGG 143
DB 72 CTCTGATTCACCTTCACTAGTATAGCATGACACTGAGGTCGCCAGAGGTCAGGAGAGG 131
QY 144 GCTGAGATGGGTCATCATCTAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 203
DB 132 GCTGAGATGGGTCATCATCTAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 191
QY 204 GAAGGGCCGATTCACATCTCCAGAGCAAGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 263
DB 192 GAAGGGCCGATTCACATCTCCAGAGCAAGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 251
QY 264 CAGCCTGAGAGCCGAGACACGAGCTGTACTACTGTGCGAGAGATTCTAGATACGATA 323
DB 252 CAGCCTGAGAGCCGAGACACGAGCTGTACTACTGTGCGAGAGATTCTAGATACGATA 311
QY 324 TTTCCTCCGTTGGGTTGCGAGCAGGATATGACGTCGTGGGGCCAAAGGACCAAGGTCAT 383

|||||
DB 312 TTTCCTCCGTTGGGATTCGAGCAGCGTATGAGACTGTGGGGCCCAAGGACACAGGTCAT 371
OY 384 CGTCTCCTCA 393
|||||
DB 372 CGTCTCCTCA 381
|||||
RESULT 3
ABS46318
ID ABS46318 standard; DNA: 311 BP.
XX
AC ABS46318;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 21308.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KM coronary heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00664.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analysing gene expression in human adult liver -
XX
PS Claim 4; SEQ ID No 21308; 658bp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (I) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABS25011-ABS11005 represent
CC human liver single exon nucleic acid probes of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 311 BP; 73 A; 75 C; 96 G; 67 T; 0 other;
Query Match 69.3%; Score 272.2; DB 23; Length 311;
Best Local Similarity 97.2%; Pred. No. 3.8e-71;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 84 CTCTGATTCACCTTCAGTACTATGATGACACTGCGGTCGCCAGGAGGAAAGG 143
|||||
DB 83 CTCTGATTCACCTTCAGTACTATGATGACACTGCGGTCGCCAGGAGGAAAGG 142
|||||
OY 144 GCTGAGTGGGTCTCATTCATTTAGTAATAGTAATATTACTTACACGACGACGT 203
|||||
DB 143 GCTGAGTGGGTCTCATTCATTTAGTAATAGTAATATTACTTACACGACGACGT 202
|||||
OY 204 GAAGGGCCGATTCACCTTCAGTACTATGATGACACTGCGGTCGCCAGGAGGAAAGG 263
|||||
DB 203 GAAGGGCCGATTCACCTTCAGTACTATGATGACACTGCGGTCGCCAGGAGGAAAGG 262
|||||
OY 264 CAGCCTGAGACCGCAGCAGCAGGCTGTACTACTTGTGCGAAGA 308
|||||
DB 263 CAGCCTGAGACCGCAGCAGCAGGCTGTACTACTTGTGCGAAGA 307
|||||
RESULT 4
ABS20923
ID ABS20923 standard; DNA: 311 BP.
XX
AC ABS20923;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon ORF from lung SEQ ID No 20914.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-234687P.
XX
PR 27-SEP-2000; 2000US-236359P.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX
PS Claim 4; SEQ ID No 20914; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a

CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human
 CC mRNA, and (b) measuring the labeled nucleic acids bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 1201 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Rudrak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC and hyaline membrane disease. The present sequence is a single exon
 CC probe open reading frame of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 311 BP; 73 A; 75 C; 96 G; 67 T; 0 other;

Query Match 69.3%; Score 272.2; DB 24; Length 311;
 Best Local Similarity 97.2%; Pred. No. 3.8e-71;
 Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 24 GGTGGAGTCTGGGGAGGCGCTGTGCAGCGCTGGGGGCTCCCTGAGACTCTCTGTGAGC 83
 DB 23 GGTGGAGTCTGGGGAGGCGCTGTGCAGCGCTGGGGGCTCCCTGAGACTCTCTGTGAGC 82
 OY 84 CTCTGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 143
 DB 83 CTCTGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 142
 OY 144 GCTGGAGTGGGTCTCATCCATTCATTAAGTATAGTATAGTATAGTATAGTATAGTATAGT 203
 DB 143 GCTGGAGTGGGTCTCATCCATTCATTAAGTATAGTATAGTATAGTATAGTATAGTATAGT 202
 OY 204 GAAGGGCGGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 263
 DB 203 GAAGGGCGGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 262
 OY 264 CAGCCTGAGAGCCGAGCAGCAGCGGTGTGTACTACTGTGCGAGAGA 308
 DB 263 CAGCCTGAGAGCCGAGCAGCAGCGGTGTGTACTACTGTGCGAGAGA 307

RESULT 5
 AAQ78959 standard; DNA: 519 BP.
 AAQ78959:
 XX 25-MAR-2003 (updated)
 DT 03-AUG-1995 (first entry)
 XX Human immunoglobulin Vh gene #21.
 DE
 XX Primer: PCR: amplify: human; immunoglobulin: variable; heavy chain;
 KW cosmid; placenta; vector; pub81; E.coli; mammalian; ds.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 11..462
 FT /*tag= a
 FT /product= human immunoglobulin variable heavy chain
 FT Intron 57..157
 FT /*tag= b
 FT misc_signal 463..465
 FT /*tag= c
 FT /note= "miscellaneous signal, does not conform to
 FT termination or splice site sequence"
 XX
 XX M09426895-A1.
 XX 24-NOV-1994.
 XX
 XX 10-MAY-1993: 93WO-JP00603.
 XX
 XX 10-MAY-1993: 93WO-JP00603.
 XX
 XX (NIBS) JAPAN TOBACCO INC.
 XX
 XX Honjo T, Matsuda F;
 XX WPI, 1995-006791/01.
 XX P-PSDB: AAR6313.
 XX
 XX DNA fragment comprising human immunoglobulin Vh genes - for the
 XX production of human immunoglobulin in mammalian hosts
 XX
 XX Claim 30: "Page 57-58; 130pp; Japanese.
 XX
 XX A series of genes (AAQ78939-79002) encoding human immunoglobulin
 XX variable heavy chains. The genes were isolated and cloned from a series
 XX of cosmid constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131,
 XX by PCR amplification using primers AAQ78917-38. The genes are subdivided
 XX into 5 families of Vh genes. The fragments cover a region of 800 kb.
 XX The DNA fragments were isolated from high molecular weight DNA from
 XX human placenta. The DNA was partially digested with Taqi restriction
 XX enzyme. The fragments were separated by gel electrophoresis and 35-45 kb
 XX cosmid vectors were isolated. The fragments were ligated with ClaI-digested
 XX cosmid vector pUBA1. The ligation products were in vitro packed and
 XX hybridised into E. coli 490A. The fragments were then subcloned by colony
 XX hybridisation. The Vh genes and the DNA fragments encoding them are
 XX useful in producing human immunoglobulin in mammalian hosts.
 XX (updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 519 BP; 123 A; 111 C; 161 G; 124 T; 0 other;

Query Match 69.3%; Score 272.2; DB 16; Length 519;
 Best Local Similarity 97.2%; Pred. No. 4.5e-71;
 Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 24 GGTGGAGTCTGGGGAGGCGCTGTGCAGCGCTGGGGGCTCCCTGAGACTCTCTGTGAGC 83
 DB 180 GGTGGAGTCTGGGGAGGCGCTGTGCAGCGCTGGGGGCTCCCTGAGACTCTCTGTGAGC 239
 OY 84 CTCTGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 143
 DB 240 CTCTGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 299
 OY 144 GCTGGAGTGGGTCTCATCCATTCATTAAGTATAGTATAGTATAGTATAGTATAGTATAGT 203
 DB 300 GCTGGAGTGGGTCTCATCCATTCATTAAGTATAGTATAGTATAGTATAGTATAGTATAGT 359
 OY 204 GAAGGGCGGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 263
 DB 360 GAAGGGCGGATTCACCTTCAGTACTATAGCATGATGCTGGTCCGCGAGGCTCCAGGAGGG 419
 OY 264 CAGCCTGAGAGCCGAGCAGCAGCGGTGTGTACTACTGTGCGAGAGA 308

DR	WP1: 2003-201468/19.
DR	P-PSDB; ABJ26763.
PT	New bispecific antibodies having antigen-binding sites specific for a
PT	first vascular endothelial growth factor (VEGF) receptor and for a
PT	second VEGF receptor, useful for inhibiting migration of leukemia
XX	cells, or for treating tumors -
PS	Disclosure: Page 70; 98pp; English.
CC	The invention relates to a novel antibody having a first antigen binding
CC	site specific for a first vascular endothelial growth factor (VEGF)
CC	receptor and a second antigen-binding site specific for a second VEGF
CC	receptor. The bispecific antigen-binding proteins block activation of the
CC	VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC	cellular functions such as angiogenesis of vascular endothelial cells
CC	and migration of leukaemia cells. The antibodies are useful for treating
CC	tumours and for in vivo or in vitro for investigative and diagnostic
CC	methods. This polynucleotide sequence represents a human DNA sequence
CC	relating to the bispecific antibodies that bind to the VEGF receptors of
CC	the invention.
SQ	Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
XX	
Query Match	68.6%; Score 269.6; DB 25; Length 348;
Best Local Similarity	96.8%; Pred. No. 2.3e-70;
Matches 275; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
OY	24 GGTCGAGCTGTGGGGAGGCGCTGATCAACCTGTGGGGGATCCTCGAGACTCTCTGTGCAGC 83
Db	12 GGTCAGTCTTGGGGAGGCGCTGTGTCMAACCCTGGGGGATCCTGAGACTCTCTGTGCAGC 71
OY	84 CTCGTGATTACCTTCAGTAGCTATAGCATCCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
Db	72 CTCGTGATTACCTTCAGTAGCTATAGCATGAACGTGGGTCCGCCAGGGTCCAGGGAAGG 131
OY	144 GCTGGAGTGGGCTCTCATCTAATAGTAATATCTTACATATATACGACGACGACGT 203
Db	132 GCTGGAGTGGGCTCTCATCTAATAGTAATATCTTACATATATACGACGACGACGT 191
OY	204 GAAGGGCCGATTCACATCTCCAGAGACAAGCCAAAGTACATCTATCTGCAATGAA 263
Db	192 GAAGGGCCGATTCACATCTCCAGAGACAAGCCAAAGTACATCTGCAATGAA 251
OY	264 CAGCCTGAGAGCCGAGCACAGCGGCTGTACTACTGTGTCGAGAG 307
Db	252 CAGCCTGAGAGCCGAGCACAGCGGCTGTATTTACTGTCTCGAGAG 295
RESULT 10	
ABT23327	
ID	ABT23327 standard; DNA; 348 BP.
XX	ABT23327;
AC	
XX	01-MAY-2003 (first entry)
DT	
XX	VEGF binding related DNA SEQ ID NO 79.
DE	
XX	Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW	leukemia cell; vascular endothelial growth factor; tumour;
KW	bispecific antigen-binding protein; human; gene; ds.
XX	Homo sapiens.
OS	
PN	WO2003002144-A1.
PD	09-JAN-2003.
XX	
PF	26-JUN-2002; 2002WO-US20332.
XX	
PR	26-JUN-2001; 2001US-301299P.
XX	

PA	(IMCL-) IMCLONE SYSTEMS INC.
PX	
PI	Zhu Z;
XX	
DR	WPI; 2003-201468/19.
XX	
PT	New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
PR	
XX	
PS	Disclosure: Page 72; 98pp; English.
XX	
CC	The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF)
CC	receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
CC	
CC	
CC	
XX	
SQ	Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
Query Match	68.6%; Score 269.6; DB 25; Length 348;
Best Local Similarity	96.8%; Pred. No. 2.3e-70;
Matches	275; Conservative 0; Mismatches 9; Indels 0; Gaps 0
OY	24 GGTGAGTCTGTGGGGAGCGCTGGTCACGCCTGGGGGTCCTTGAGACTCTCCTGTCAGC 83 12 GTTGCAGCTGTGGGGAGCGCTGTGCAAGCCTGGGGGTCCTTGAGACTCTCCTGTCAGC 71
DB	
OY	84 CTCGTGATTACACCTTCAGTAGCATATGACATGCACTGGGTGCCGACAGGTTCCAGGAAGG 143 72 CTCTGGAATTCACCTTCAGTAGCATATGACATGCACTGGGTGCCGACAGGTTCCAGGAAGG 131
DB	
OY	144 GCTGAGATGGGCTCATCATTAATAAATAAATACTTACATATACTACAGACGACAGT 203 132 GCTGAGATGGGCTCATCATTAATAAATAAATACTTACATATACTACAGACGACAGT 191
DB	
OY	204 GAAGGCGCGATTACCATTCTCCAGAGACAAGCCCAAGAAGCTCACTGTATCTTCAATGAA 263 192 GAAGGCGCGATTACCATTCTCCAGAGACAAGCCCAAGAAGCTCACTGTATCTTCAATGAA 251
OY	264 CAGCCTGAGAGCCGAGCACACAGCGCTGTACTACTACTGTGCGAGAG 307 252 CAGCCTGAGAGCCGAGCACACAGCGCTGTACTACTACTGTGCGAGAG 295
DB	
RESULT 11	
ABS62722	
ID	ABS62722 standard; DNA; 376 BP.
XX	
AC	ABS62722;
DT	24-OCT-2002 (first entry)
XX	
DE	Anti-IGF-IR antibody VH chain DNA consensus sequence #1.
XX	
KM	Insulin-like growth factor I receptor; antibody; human; ds; gene;
KM	cytostatic; osteoporosis; anti-neoplastic; anti-tumour; anti-angiogenic;
KM	neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
XX	atherosclerosis.
OS	Homo sapiens.
XX	
FN	WO200253596-A2.
PD	11-JUL-2002.

XX 20-DEC-2001; 2001WO-US51113.
 XX
 XX 05-JAN-2001; 2001US-259927P.
 XX
 XX (PFIZ) PFIZER INC.
 XX (ABGE-) ABGENIX INC.
 XX
 XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX
 XX MPI: 2002-575410/61.
 XX
 XX Novel humanized, chimeric monoclonal antibody that specifically binds
 XX to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 XX binding of IGF-I or IGF-II to receptor and for treating cancer in
 XX humans
 XX
 XX Disclosure: Figure 2A; 172pp; English.
 XX
 XX This invention relates to a novel humanised, chimeric or human
 XX monoclonal antibody or its antigen binding portion that specifically
 XX binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
 XX of the invention can act as an inhibitor of binding of IGF-I or IGF-II
 XX with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 XX phosphorylation. The antibodies of the invention are useful for
 XX diagnosing the presence or location of an IGF-IR-expressing tumour in a
 XX subject. The antibody or its antigen-binding portion is also useful for
 XX treating cancer in a human. The method for this further involves an anti
 XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
 XX The antibodies may also be useful for increasing IGF-IR activity and
 XX thus restoring IGF-IR activity in a condition characterised by low
 XX IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
 XX invention is also useful for inducing apoptosis of specific cells in a
 XX patient, and to treat non-cancerous states or disease, e.g. acromegaly,
 XX gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
 XX antibodies minimise the immunogenic and allergic responses intrinsic to
 XX mouse or mouse-derivatised monoclonal antibodies and thus increase the
 XX efficacy and safety of the administered antibodies. The present sequence
 XX represents a DNA sequence encoding an anti-insulin-like growth
 XX factor I receptor antibody of the invention.
 XX
 XX Sequence 376 BP; 87 A; 91 C; 110 G; 82 T; 6 other;

Query Match 68.4%; Score 268.8; DB 24; Length 376;
 Best Local Similarity 83.8%; Pred. No. 4,1e-70;
 Matches 310; Conservative 6; Mismatches 48; Indels 6; Gaps 1;

QY 24 GGTGAGTCTGGGGGAGGCGCTGGTCAAGCCTGGGGGCTCTGAGACTCTCTGTCAGC 83
 DB 12 GGTGAGTCTGGGGGAGGCGCTGGTCAAGCCTGGGGGCTCTGAGACTCTCTGTCAGC 71
 QY 84 CTCGTGATTCACCTTCATAGCTATAGCATGCTGGTCCGCCAGGGTCCAGGAAAGG 143
 DB 72 CTCGTGATTCACCTTCATAGCTATAGCATGCTGGTCCGCCAGGGTCCAGGAAAGG 131
 QY 144 GCTGAGTGGCTCTCATCATTAATAGTAATATACATATACATACGACGCACT 203
 DB 132 GCTGAGTGGCTCTCATCATTAATAGTAATAGTAATACCAKAKACACGACGCTGCT 191
 QY 204 GAAGGCGCGATTCACCATCTCCAGAGACGCGCAAGCAACTGATATCTGCAATGAA 263
 DB 192 GAAGGCGCGATTCACCATCTCCAGAGACGCGCAAGCAACTGATATCTGCAATGAA 251
 QY 264 CAGCTGAGAGCCGAGCAGCGCTGTGTACTAGTGTGAGAAATCTTAGATACAGTA 323
 DB 252 CAGCTGAGAGCCGAGCAGCGCTGTGTACTAGTGTGAGAAATCTTAGATACAGTA 311
 QY 324 TTTCTCCGTTGGGTTGCGAGCAGCGATAGACGTGGGGCCAAAGGACCAAGGTCAT 383
 DB 312 TTT-----TTACTACTACTACTAGGATAGGAGCTGTGGGGCCAAAGGACCAAGGTCAC 365
 QY 384 CGTCTCTCTCA 393
 |||||||||

DB 366 CGTCTCTCTCA 375
 RESULT 12
 ID AAD46294
 XX AAD46294 standard; DNA; 348 BP.
 AC AAD46294;
 XX
 XX 27-DEC-2002 (first entry)
 DE Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
 XX
 XX Human: tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
 KW VH; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 1..348
 FT /*tag= a
 FT /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
 FT protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 XX W0200270008-A1.
 XX
 XX 12-SEP-2002.
 XX
 XX 04-MAR-2002; 2002WO-US06762.
 XX
 XX 02-MAR-2001; 2001US-0798689.
 XX
 XX (IMCL-) IMCLONE SYSTEMS INC.
 XX (ROCK/) ROCKWELL P.
 XX (GOLD/) GOLDSTEIN N I.
 XX
 XX MPI: 2002-691738/74.
 DR P-PSDB: AAE28873.
 XX
 XX Inhibiting tumor growth in humans involves administering vascular
 XX endothelial growth factor receptor antagonists in combination with
 XX radiation, chemotherapeutic agents, or epidermal growth factor receptor
 XX antagonists
 XX
 XX Example 12; Page 126; 151pp; English.
 XX
 XX The invention relates to a method of inhibiting tumour growth which
 XX involves administering vascular endothelial growth factor receptor
 XX (VEGFR) antagonists in combination with radiation, chemotherapeutic
 XX agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 XX is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 XX tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 XX kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 XX bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 XX expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 XX or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 XX It is preferably useful for treating subjects with both solid tumours,
 XX preferably high vascular tumours and non-solid tumours. The inhibition
 XX or reduction of tumour growth includes prevention or inhibition of the
 XX progression of tumour, including cancerous and non-cancerous tumours,
 XX where the progression of tumours includes the invasiveness, metastasis,
 XX recurrence and increase in size of the tumour. The present sequence is
 XX human KDR (VEGFR-2) Fab antibody heavy chain DNA.
 XX
 XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
 Query Match 68.2%; Score 268; DB 24; Length 348;
 Best Local Similarity 96.5%; Pred. No. 7e-70;
 Matches 274; Conservative 0; Mismatches 10; Indels 0; Gaps 0;


```

PR 17-NOV-1997; 97EP-0120096.
XX
XX (KUFE/) KUFE P.
XX
XX Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;
XX WPI: 1999-338004/28.
XX P-PSDB; AAV17954.
XX
XX Phage display system for identification of binding site domains
XX retaining capacity to bind an epitope
XX
XX Dislosure; Fig 3.1; 152pp; English.
XX
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX *diagnostically, for e.g. cancer and autoimmune diseases. Scrv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method.
XX
XX Sequence 381 BP; 87 A; 93 C; 120 G; 81 T; 0 other:
SQ
Query Match 66.5%; Score 261.2; DB 20; Length 381;
Best Local Similarity 81.6%; Pred. No. 7.6e-68;
Matches 302; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCGCTGGGGGTCCTGAGACTCTCTGTGCAGC 83
DB 12 GCTCGAGTCTGGGGAGGCGGTGTGTCAGCGCTGGGGTCTCTGAGACTCTCTGTGCAGC 71
QY 84 CTCTGGATTACACTTCAGTAGCTATAGCATGCACATGCGGTCCGCCAGGGTCCAGGGAAGG 143
DB 72 CTCTGGATTACACTTCAGTAGCTATAGCATGCACATGCGGTCCGCCAGGGTCCAGGGAAGG 131
QY 144 GCTGAGTGGGTCTCTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 203
DB 132 GCTGAGTGGGTCTCTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 191
QY 204 GAAGGCCGATTACCATCTCCAGAGACAGCAAGCAACTCAGCTATCTGCAATGAA 263
DB 192 GAAGGCCGATTACCATCTCCAGAGACAGCAATTCGAAGACAGCTGTATCTTCAATGAA 251
QY 264 CAGCTGAGAGCCGAGACACAGCGCTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
DB 252 CAGCTGAGAGCCGAGACACAGCGCTGTATTAAGTATGAGAAATATGGGTGGGGCAG 311
QY 324 TTCTCTCCGTTGGGTTCGAGGAGCATGAGCTGTGGGCCAAGGACACGCTCAT 383
DB 312 TGGCTGGAGAGCCCTACTACTACTAGCATGATGAGCTGTGGGGCCAAAGGACACGCTCAC 371
QY 384 GCTCTCTCA 393
DB 372 GCTCTCTCA 381

RESULT 17
AAV68537
ID AAV68537 standard; DNA; 414 BP.
XX
XX AAV68537;
XX

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DT 16-FEB-1999 (first entry)
XX
XX Nucleotide sequence of human D4.5 heavy chain variable region.
XX
XX Human; D4.5 heavy chain variable region; receptor; antigen;
XX tumour; auto-immune disease; graft rejection; allergy;
XX inflammatory disease; endocrine disease; degenerative disease; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..414
XX FT /*tag=^a
XX FT /product= "human D4.5 heavy chain variable
XX FT region"
XX
XX WO9846645-A2.
XX
XX 22-OCT-1998.
XX
XX 14-APR-1998; 98WO-EP02180.
XX
XX 14-APR-1997; 97EP-0106109.
XX
XX (KUFE/) KUFE P.
XX (RAUM/) RAUM T.
XX
XX Kufer P, Raum T;
XX
XX WPI: 1998-594564/50.
XX P-PSDB; AAW80815.
XX
XX Production of anti-human antigen receptors - by selecting a
XX combination of functionally rearranged VH and VL immunoglobulin
XX chains expressed from a recombinant vector
XX
XX Claim 9; Fig 7; 84pp; English.
XX
XX This is the nucleotide sequence of the human D4.5 heavy chain
XX variable region, used in the method of the invention, for providing
XX receptors that can be used for targeting antigens in humans without
XX being immunogenic themselves. Such receptors can be used for treating
XX diseases such as tumours or auto-immune diseases, graft rejection
XX after transplantation, infectious diseases by targeting cellular
XX receptors as well as allergic, inflammatory, endocrine and
XX degenerative diseases by targeting key molecules involved in the
XX pathological process.
XX
XX Sequence 414 BP; 93 A; 106 C; 127 G; 88 T; 0 other:
SQ
Query Match 66.5%; Score 261.2; DB 19; Length 414;
Best Local Similarity 81.6%; Pred. No. 7.8e-68;
Matches 302; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCGCTGGGGGTCCTGAGACTCTCTGTGCAGC 83
DB 12 GCTCGAGTCTGGGGAGGCGGTGTGTCAGCGCTGGGGTCTCTGAGACTCTCTGTGCAGC 71
QY 84 CTCTGGATTACACTTCAGTAGCTATAGCATGCACATGCGGTCCGCCAGGGTCCAGGGAAGG 143
DB 72 CTCTGGATTACACTTCAGTAGCTATAGCATGCACATGCGGTCCGCCAGGGTCCAGGGAAGG 131
QY 144 GCTGAGTGGGTCTCTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 203
DB 132 GCTGAGTGGGTCTCTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 191
QY 204 GAAGGCCGATTACCATCTCCAGAGACAGCAAGCAACTCAGCTATCTGCAATGAA 263
DB 192 GAAGGCCGATTACCATCTCCAGAGACAGCAATTCGAAGACAGCTGTATCTTCAATGAA 251
QY 264 CAGCTGAGAGCCGAGACACAGCGCTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
DB 252 CAGCTGAGAGCCGAGACACAGCGCTGTATTAAGTATGAGAAATATGGGTGGGGCAG 311

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heavy chain) and the other chain comprises C κ -domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteromimipolypeptides have cytoskeletal, immunostimulatory, antileukaemic and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

The present sequence is a DNA encoding left chain of a heteromimibody comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to human CH1 domain which bears at its C-terminus the human inflammatory cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus a hexahistidine sequence for ease of purification. HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

SQ Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 other;

Query Match 66.28; Score 260.2; DB 21; Length 1630;

Best Local Similarity 81.6%; Pred. No. 2.4e-67;

Matches 301; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY	24	GGTGGAGTCTGGGGGAGGCGCTGGTCAAGCCTTGGGGGGTCCCTGAGACTCTCTCTGAC	83
Db	473	GCTCGAGTCTGGGGGGAGGGGTGCACCTCTGGGAGTCCCTGAGACTCTCTCTGGAGC	532
QY	84	CTTGGATTACACCTTAGTAGCTATAGCATGCACATGGGTCCGCCAGGGTCCAGGAAGGG	143
Db	533	CTGTGGATTACCTTCAGTAGTAGCATGCACATGGGTCCGCCAGGGTCCAGGAAGGG	592
QY	144	GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATCTTACATATACACGACGACGT	203
Db	593	GCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATATACTATGACAGCTCGT	652
QY	204	GAGGGGCGCATTTACACATCTCCAGAGACACAGCCCAAGAACTACTGTTCTGCAATGAA	263
Db	653	GAGGGGCGCATTTACACATCTCCAGAGACAAATTCCAAGAACGCTGTATCTGCAAAATGAA	712
QY	264	CACCTTAGAGCGCAGACACAGCGCTGTACTACTGTCGAGAGATTTCTAGATACAGTAA	323
Db	713	CACCTTAGAGCGCTGAGGAGACACGGCTGTATTACTGTCTCGAAAGATATGGGGTGGGCGAG	772
QY	324	TTTTCTCCGTTGGGTTCCGAGCGACGGATATGAGACTCTGGGGCCAAAGGACACAGTCAT	383
Db	773	TGCGTGGAGACCTTACTACTACTAGCATGTATGAGACTCTGGGGCCAAAGGACACAGTCCAC	832
QY	384	CGTCTCCTC 392	
Db	833	CGTCTCCTC 841	

```

RESULT 20
AAZ50588
ID    AAZ50588 standard; DNA; 1630 BP.

```

AC AAZ50588;

DT 23-MAY-2000 (first entry)

DE HD70scfv-Ck-Interleukin 2 encoding DNA

KM HD70; single-chain variable fragment; scFv; 17-1A antigen; human;
 KM EPCAM; epithelial cell adhesion molecule; inflammatory cytokine;
 KM IL-2; interleukin-2; Ck-domain; kappa light chain constant domain;
 KM heteromultibody; multifunctional compound; immunoglobulin;
 KM cytotoxic; immunostimulatory; anti-leukemia; diagnosis; prevention;
 KM antiproliferative; treatment; malignant; hematopoietic cell;
 KM leukemia; solid tumour; carcinoma; melanoma; sarcoma; ds.

OS Homo sapiens.

XX		Location/Qualifiers
FH	Key	39..1613
FT	CDS	
FT		/*tag= a
FT		/Product= "HD70scFv-CK-IL-2 chain"
FT	misc_feature	96..342
FT		/*tag= b
FT		/label= HD70_scFv
FT		

PN WO200006605-A2

PD 10-FEB-2000

PF 28-JUL-1999; 99WO-EP05416.

PR 28-JUL-1998; 98EP-0114082.

PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

PI Kufer P, Dreier T, Baueerle PA, Borschert K, Zettl F;

DR WPI; 2000-195265/17.

XX
XX

PT malignant cell growth and for detection and diagnosis -

PS Claim 8; Fig 55B; 166pp; English.

The patent discloses heteroinhibitors which are multifunctional compounds producible in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises, a CH1 domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (polypeptides having different receptor or ligand functions, where further at least two of the different (polypeptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteroinhibitors have cytostatic, immunostimulatory, antileukemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

The present sequence is a DNA encoding right chain of a heteroinhibitor comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to human Ck domain (constant domain of immunoglobulin-kappa light chain) which bears at its C-terminus the human inflammatory cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.

SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 other.

Query Match 66.28; Score 260.2; DB 21; Length 1630

Best Local Similarity 81.6%; Pred. No. 2.4e-67;

Matches 301; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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Db	473	GCTCGAGATCTGGGGGGAGGGGTGGTCCAGCGCTTGGGAGGCTCCGTGAGACTCTCTCTGTGACG	532
QY	84	CTCTGGAATTCACCTTCTAGTAGCATTATAGCATGTCAGTCAGTGGGTCTCCGACAGGGTCCAGGGAAGG	143
Db	533	CTCTGGAATTCACCTTCTAGTAGCATTATAGCATGTCAGTCAGTGGGTCTCCGACAGGGTCCAGGGAAGG	592
QY	144	GCTGGAGTGGGCTCATCCATTAGTAATAGTAATATCTTACATATTACTACGACGACGAGT	203
Db	593	GCTGGAGTGGGCTCATCCATTATATCATATATGATGGAAGTAATTAATTAATCATGACGACCTCGT	652
QY	204	GAGGGGCGCATTCACCATCTCCAGAGACAAGCCCAAGCAATCCTACTGTAATTCGCAAAATGAA	265
Db	712	GAGGGGCGCATTCACCATCTCCAGAGACAATTCCAAGCAAGCTGTATCTGCAAAATGAA	712

OY	264	CAGCCTGAGAGCCGAGACACGCGTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA	323
Db	713	CAGCCTGAGAGCTGAGAGACGCGTGTGTATTACTGTGCGAAGATATGGGGGCGNG	772
OY	324	TTTCCCTCCGTTGGGTTGCGAGCGAGGTATGGAGCTGTGGGCCAAGGACCACGGTCAT	383
Db	773	TGGCTGGAGACCCCTACTACTACTACGATGAGCGTCTGGGGCCAAAGGACCACGGTCAC	832
OY	384	CGTCTCCTC	392
Db	833	CGTCTCCTC	841

Search completed: September 24, 2003, 03:27:35
job time : 271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2003, 02:42:43 ; Search time 2280 Seconds
(without alignments)
4189.324 Million cell updates/sec

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Perfect score: 393
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Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estrov:*
6: em_esttpl:*
7: em_esttro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	302.8	77.0	740	10	BG757947 602114983
2	302.8	77.0	741	10	BG754024 602709552
3	283.6	72.2	875	13	BQ706723 AGENCOURT
4	283.6	72.2	968	13	BQ706746 AGENCOURT

5	282	71.8	889	13	BX357384
6	281.8	71.7	1004	13	BQ711355 AGENCOURT
7	277.8	70.7	1010	13	BQ711025 AGENCOURT
8	273.2	69.5	687	10	BG397964
9	270	68.7	1069	12	BM914329
10	268.2	68.2	471	9	AW403220
11	268.2	68.2	908	10	BG686881
12	267.4	68.0	397	9	AW403886
13	266.8	67.9	1138	13	BX379829
14	266.8	67.9	1201	13	BX417408
15	264	67.2	447	9	AW402793
16	263.2	67.0	738	10	BG340686
17	258.4	65.8	613	12	BM007475
18	258.4	65.8	879	10	BG759748
19	257.4	65.5	890	13	BQ709879
20	256.8	65.3	443	9	AW401428
21	256.6	65.3	804	10	BG754761
22	255.6	65.0	1194	13	BX359679
23	255.2	64.9	911	13	BQ712666
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25	255	64.9	988	13	BQ712092
26	254	64.6	445	9	AW408316
27	254	64.6	876	10	BG758406
28	253.6	64.5	618	12	BM713479
29	252	64.1	326	10	BE156045
30	251.2	63.9	530	12	BM819424
31	250.8	63.8	669	10	BG686716
32	250.6	63.8	471	12	BM848820
33	250.6	63.8	556	12	BM820006
34	250.6	63.8	567	12	BM820534
35	250.6	63.8	640	12	BM819504
36	250.6	63.8	686	12	BM849368
37	250.6	63.8	801	13	BX399298
38	250.4	63.7	792	10	BE129047
39	250	63.6	823	10	BE547512
40	249.6	63.5	1164	10	BE974771
41	249	63.4	932	13	BQ711605
42	248.4	63.2	390	9	AW408285
43	248.2	63.2	440	9	AW408304
44	248	63.1	406	9	AW401971
45	247.4	63.0	705	10	BG758682
46	247.2	62.9	942	13	BQ710859
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48	246.6	62.7	979	13	BQ708029
49	246.4	62.7	378	9	AA740786
50	246.4	62.7	859	13	BX368110
51	246.2	62.6	860	13	BQ705956
52	246	62.6	456	9	AW403059
53	245.4	62.4	902	12	BM007556
54	245	62.3	481	14	CA397706
55	244.8	62.3	894	13	BQ708235
56	244.6	62.2	436	12	BM820963
57	244.4	62.2	516	9	AW401728
58	244.4	62.2	973	10	BG397895
59	244.4	62.2	984	13	BQ709776
60	244	62.1	964	13	BQ708077

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	740 bp	mRNA	linear	EST 15-MAY-2001
BG757947	602714983P1	NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854932 5'				
ACCESSION	BG757947	mRNA sequence.				
VERSION	BG757947.1	GI:14068600				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Eutheria; Primates; Catarrhini; Homidae; Homo.					

REFERENCE	1 (bases 1 to 740)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LILCM1703 row: f column: 21
 High quality sequence stop: 736.
 Location/Qualifiers

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/clone="IMAGE:4654932"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC library."

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BASE COUNT	166 a	203 c	206 g	165 t	
ORIGIN					
Query Match	77.08;	Score 302.8;	DB 10;	Length 740;	
Best Local Similarity	88.68;	Pred. No. 9,4e-73;			
Matches 320;	Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;
Db	24	GGTGGAGTCTGGGGGAGCGCTGTCAAGCCCTGGGGGCTCCCTGAGACTCTCTGTGCAGC	83		
QY	92	GGTGGAGTCTGGGGGAGCGCTGTGTGACGCCCTGGGGGCTCCCTGAGACTCTCTGTGCAGC	151		
Db	84	CTCTGGATTCACCTTCAGTAGCTATATAGACAGCACTGGTCCGACGAGGTCCAGGAGAGG	143		
QY	152	CTCTGGATTCACCTTCAGTAGCTATATAGACAGCACTGGTCCGACGAGGTCCAGGAGAGG	211		
Db	144	GGTGGAGTGGGTCTCATACCATTTAGTATATAGTATTAATACTATATCTATACGACAGCGAGT	203		
QY	212	GGTGGAGTGGGTCTCATACCATTTAGTATATAGTATTAATACTATATCTATACGACAGCGAGT	271		
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QY	272	GAGGGGCGCATTCACCATCTCCAGAGACAGCAAGCCAGCAACCTGATATGCAAAATGAA	331		
Db	264	CACCTTGAGACCGGACAGACAGCGCTGTGCTACTACTGTGCGAGAGATTCTGATACAGTAA	323		
QY	332	CACCTTGAGACCGGACAGACAGCGCTGTGCTACTACTGTGCGAGAGATTCTGATACAGTAA	391		
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QY	392	TACTACCAAGTGGTACTACTACTACTACGATATGAGAGCTGTGGGGCCAAAGGACCAAGCAT	451		
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LOCUS	BG754024				
DEFINITION	602709552n1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846117 5',				

ACCESSION	BCG754024	GI:14064677
VERSION	BCG754024.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (pages 1 to 741)
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished
	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 Sequencing by: Incyte Genomics, Inc.
 Additional Information can be found at:
<http://image.llnl.gov>
 Plate: LICM1686 row: 9 column: 14
 High quality sequence stop: 735.

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Location/Qualifiers
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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC_48"
/ote="Organ: B-cells; Vector: pOTR7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGCG(s). Size-selected >500bp
for average insert size 1.8kb. Library constructed by J.
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC library."
BASE COUNT
166 a 204 c 206 g 165 t

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Query Match:	77.0%	Score 302.8:	DB 10:	Length 741:
Best Local Similarity:	88.6%	Pred. No. 9,4e-73:		
Matches 328:	Conservative	0:	Mismatches 42:	Indels 0:
			Gaps	0:
QY	24	GGTGGAGTCCTGGGGGAGGCGCTGTGCACAGCCTGGGGGGTCCCTAGACCTCTGCTGGACAC	83	
Db	92	GGTGGAGTCCTGGGGGAGGCGCTGTGCACAGCCTGGGGGGTCCCTAGACCTCTGCTGGACAC	151	
QY	84	CTCTGTGATTCACCTTTCAGTACCTATTCACATGTACACTGGTGTCCGCAGAGTCCAGGGAGGG	143	
Db	152	CTCTGTGATTCACCTTTCAGTACCTATTCACATGTACACTGGTGTCCGCAGAGTCCAGGGAGGG	211	
QY	144	GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATTAATACGACAGCCAGCT	203	
Db	212	GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATTAATACGACAGCTCTGT	271	
QY	204	GAAGGGCCGATTACCATCTTCCAGAGACAAGGCCAAGACCTCACTGTATCTGCCAATGAA	263	
Db	272	GAAGGGCCGATTACCATCTTCCAGAGACAAGGCCAAGACCTCACTGTATCTGCCAATGAA	331	
QY	264	CAGCCTGAGAGCCAGAGCACAGCGGTGTCTACTCTGTGGAGAGATTCTAGATACAGTAA	323	
Db	332	CAGCCTGAGAGCCAGAGCACAGCGGTGTCTACTCTGTGGAGAGATTCTAGATACAGTAA	391	
QY	324	TTTCTCTCGTGGGGTTTGGAGCGAGCGTATAGACGCTCTGGGGCCAAAGGACACCGGTAT	383	
Db	392	TAGTACCGACGCTACTACTACTACGGTATAGACGCTCTGGGGCCAAAGGACACCGGTATC	451	
QY	384	CGTCTCCTCA	393	

Db 452 CGTCTCTCA 461
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LOCUS B0706723 875 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7977332 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6215779
5', mRNA sequence.
ACCESSION B0706723
VERSION B0706723.1 GI:21845622
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2385 row: d column: 20
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/note="Organ: spleen; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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Matches 316; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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DB 134 GGTGAGTCTGGGGAGGCGCTGTCAGCCTGGGGGTCCTGAGACTCTCTGTGCAC 193
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QY 84 CTCTGAGTTCACCTTCAGTAGTATAGATGATGCTGGGTCGCCAGGGTCCAGGAAGG 143
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QY 324 TTTCCTCGGTGGGTTCCGAGCGAGTATGAGACTGTGGGCGCAAGGACCGGTCAAT 383
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QY 384 CGTCTCTCA 393
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VERSION B0706746.1 GI:21845645
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 968)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/note="Organ: spleen; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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Query Match 72.2%; Score 283.6; DB 13; Length 968;
Best Local Similarity 85.4%; Pred. No. 2.1e-67; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGCCTGGGGGTCCTGAGACTCTCTGTGCAC 83
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Db      315 GAGGGCCGATTCACCATCTCCAGACAAACGCAAGCTGATTTGCCAAATGAA 374
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Qy      324 TTTCCTCCGTTGGGTTGGAGGACGATGTGGAGCGTGGGCGCAAGGAGCCAGTCAAT 383
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Qy      384 CGTCTCCCTCA 393
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DEFINITION
ACCESSION BX357384
VERSION    BX357384.1 GI:30366120
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ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS   Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT    Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI025C050P1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI025C050P1.
FEATURES
Source
Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
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sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 200 a 252 c 251 g 184 t
ORIGIN
Query Match 71.8%; Score 282; DB 13; Length 889;
Best Local Similarity 87.3%; Pred. No. 5,7e-67;
Matches 323; Conservative 0; Mismatches 40; Indels 7; Gaps 1;

Qy      24 GGTGAGTCTGGGGAGGAGGCTGTGCAAGCTGGGGGCTCCTGAGACTCTCCTGTGACG 83
Db      179 GGTGAGTCTGGGGAGGAGGCTGTGCAAGCTGGGGGCTCCTGAGACTCTCCTGTGACG 238
Qy      84 CTCTGATTCACCTTCAGTAGATATAGCATGATGATGCTCCGCGAGGGTCCAGGAAAGG 143
Db      239 CTCTGATTCACCTTCAGTAGATATAGCATGATGATGCTCCGCGAGGGTCCAGGAAAGG 298
Qy      144 GGTGAGTGGTCTCATCTAGTAATAGTAATCTTACATATCTCTAGCGAGAGCGCAGT 203

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Db      299 GCTGAGTGGGTTTCATCATTAAGTAGTAGTAGTAGTACATATACTACGACAGACTGTGT 358
Qy      204 GAGGGCCGATTCACCATCTCCAGAGACAAACGCAAGCTGATCTGCAAAATGAA 263
Db      359 GAGGGCCGATTCACCATCTCCAGAGACAAACGCAAGCTGATCTGCAAAATGAA 418
Qy      264 GAGCCTGAGAGCCGAGACACAGGCTGTGTACTGTGGAGAGATTCTAGATACAGTAA 323
Db      419 GAGCCTGAGAGCCGAGACACAGGCTGTGTACTGTGGAGAGATTCTAGATACAGTAA 471
Qy      324 TTTCCTCCGTTGGGTTGGAGGACGATGTGGAGCGTGGGCGCAAGGAGCCAGTCAAT 383
Db      472 TTGGCGCAGGTGTGTACACCTGTGAGCGTATGTGAGCTGTGGGCGCAAGGAGCCAGTCAAT 531
Qy      384 CGTCTCCCTCA 393
Db      532 CGTCTCCCTCA 541

RESULT 6
BX711355 1004 bp mRNA linear EST 16-JUL-2002
LOCUS    BX711355
DEFINITION
ACCESSION AGENCOURT.8353131 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278123
VERSION    BX711355
KEYWORDS   5', mRNA sequence.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1004)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LICM2465 row: j column: 12
High quality sequence stop: 486.
FEATURES
Source
Location/Qualifiers
1..1004
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278123"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(5). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT 217 a 299 c 279 g 209 t
ORIGIN
Query Match 71.7%; Score 281.8; DB 13; Length 1004;
Best Local Similarity 86.6%; Pred. No. 6,9e-67;
Matches 323; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Qy      24 GGTGAGTCTGGGGAGGAGGCTGTGCAAGCTGGGGGCTCCTGAGACTCTCCTGTGACG 83
Db      130 GGTGAGTCTGGGGAGGAGGCTGTGCAAGCTGGGGGCTCCTGAGACTCTCCTGTGACG 189

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QY 84 CTCGTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
 DB 190 CTCGTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 249
 QY 144 GCTGAGAGTGGGCTCTATCCATTAGTAATAGTAATCTTACATATCTACGACGACGCACT 203
 DB 250 GCTGAGAGTGGGCTCTATCCATTAGTAATAGTAATCTTACATATCTACGACGACGCACT 309
 QY 204 GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACATCATGTATCTGCAATGAA 263
 DB 310 GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACATCATGTATCTGCAATGAA 369
 QY 264 CAGCCTGAGAGCCGACAGCAGCGCTGTACTACTGTGAGAGATTTCTAGATACAG-- 320
 DB 370 CAGCCTGAGAGCCGACAGCAGCGCTGTACTACTGTGAGAGATTTCTAGATACAG-- 429
 QY 321 TAATTTCTCCGTTGGGTTCCGAGGCGACGATGAGCTCTGGGCCAAGGACCAACGCT 380
 DB 430 ACTATGTTCCGGGGGCGACAATATATGATCTTTGATATCTGGGGCCCAAGGACCAATGCT 489
 QY 381 CATGCTTCCTCA 393
 DB 490 CACGCTCTCTCA 502

RESULT 7
 LOCUS B0711025 1010 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT_7983315 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215468
 5', mRNA sequence.
 B0711025
 B0711025.1 GI:21849924

ACCESSION
 VERSION B0711025
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1010)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2384 row: g column: 21
 High quality sequence stop: 358.

FEATURES
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 Location/Qualifiers
 1..1010
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6215468"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOT87; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 202 a 301 c 272 g 235 t
 ORIGIN

Query Match 70.7%; Score 277.8; DB 13; Length 1010;
 Best Local Similarity 84.6%; Pred. No. 8.7e-66;

Matches 312; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGGCTGGGGGGTCCCTGAGACTCTCTGGACGC 83
 DB 135 GGTGAGTCTGGGGAGGCGCTGTCAGGCTGGGGGGTCCCTGAGACTCTCTGGACGC 194
 QY 84 CTCGTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
 DB 195 CTCGTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 254
 QY 144 GCTGAGAGTGGGCTCTATCCATTAGTAATAGTAATCTTACATATCTACGACGACGCACT 203
 DB 255 GCTGAGAGTGGGCTCTATCCATTAGTAATAGTAATCTTACATATCTACGACGACGCACT 314
 QY 204 GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACATCATGTATCTGCAATGAA 263
 DB 315 GAAGGGCCGATTCACCATCTCCAGAGACAGCCCAAGAACATCATGTATCTGCAATGAA 374
 QY 264 CAGCCTGAGAGCCGACAGCAGCGCTGTACTACTGTGAGAGATTTCTAGATACAGTA 323
 DB 375 CAGCCTGAGAGCCGACAGCAGCGCTGTACTACTGTGAGAGATTTCTAGATACAGTA 434
 QY 324 TTTCTCCGTTGGGTTCCGAGGCGACGATGAGCTCTGGGCCAAGGACCAACGCTCA 383
 DB 435 CCATATTTTGAAGTCTGTTGCTTAAGAACTGACTACTGGGGCCAGGGAACCTGCTCA 494
 QY 384 CAGCTTCCTC 392
 DB 495 CAGCTTCCTC 503

RESULT 8
 LOCUS BG397964 687 bp mRNA linear EST 12-MAR-2001
 DEFINITION 602439484F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565804 5',
 mRNA sequence.
 BG397964
 BG397964.1 GI:13291412

ACCESSION
 VERSION BG397964
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 687)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Straub, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1283 row: g column: 21
 High quality sequence stop: 673.

FEATURES
 source
 Location/Qualifiers
 1..687
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4565804"
 /lab_host="Primary B-cells from tonsils (cell line)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOT87; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT
ORIGIN

147 a 189 c 197 g 154 t

Query Match 69.5%; Score 273.2; DB 10; Length 687;
Best Local Similarity 97.2%; Pred. No. 1,3e-64;
Matches 278; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAAGCTTGGGGGCTCCGAGACTCTCTGTGCACG 83
DB 116 GTGGAGTCTGGGGAGGCGCTGTCAAGCTTGGGGGCTCCGAGACTCTCTGTGCACG 175
QY 84 CTCTGATTACCTTCACTAGTACTATAGCATGCACTGGTCCGCGAGGTCACAGGAAGG 143
DB 176 CTCTGATTACCTTCACTAGTACTATAGCATGCACTGGTCCGCGAGGTCACAGGAAGG 235
QY 144 GCTGAGTGGGTCTCATCTTCACTAGTAAATAGTAACTATACATATACAGCAGACGACT 203
DB 236 GCTGAGTGGGTCTCATCTTCACTAGTAAATAGTAACTATACATATACAGCAGACGACT 295
QY 204 GAAGGCGCATTCACATCTCCAGAGACACGCCAAGACATCATCTATCTGCAATGAA 263
DB 296 GAAGGCGCATTCACATCTCCAGAGACACGCCAAGACATCATCTATCTGCAATGAA 355
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGGAGAGAT 309
DB 356 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGGAGAGAT 401

RESULT 9
LOCUS BM914329 1069 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6615320 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:5479996
5', mRNA sequence.
ACCESSION BM914329
VERSION BM914329.1 GI:19364708
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1069)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
plate: LNCM2002 row: c column: 05
High quality sequence stop: 556.

FEATURES
source

1. 1069
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5479996"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOMB; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a

NIH-MGC Library."
BASE COUNT 268 a 362 c 262 g 176 t 1: others
ORIGIN

Query Match 68.7%; Score 270; DB 12; Length 1069;
Best Local Similarity 96.5%; Pred. No. 1,3e-63;
Matches 276; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAAGCTTGGGGGCTCCGAGACTCTCTGTGCACG 83
DB 126 GTGGAGTCTGGGGAGGCGCTGTCAAGCTTGGGGGCTCCGAGACTCTCTGTGCACG 185
QY 84 CTCTGATTACCTTCACTAGTACTATAGCATGCACTGGTCCGCGAGGTCACAGGAAGG 143
DB 186 CTCTGATTACCTTCACTAGTACTATAGCATGCACTGGTCCGCGAGGTCACAGGAAGG 245
QY 144 GCTGAGTGGGTCTCATCTTCACTAGTAAATAGTAACTATACATATACAGCAGACGACT 203
DB 246 GCTGAGTGGGTCTCATCTTCACTAGTAAATAGTAACTATACATATACAGCAGACGACT 305
QY 204 GAAGGCGCATTCACATCTCCAGAGACACGCCAAGACATCATCTATCTGCAATGAA 263
DB 306 GAAGGCGCATTCACATCTCCAGAGACACGCCAAGACATCATCTATCTGCAATGAA 365
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGGAGAGAT 309
DB 366 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGGAGAGAT 411

RESULT 10
LOCUS AW403220 471 bp mRNA linear EST 16-FEB-2000
DEFINITION UT-HF-BK0-aay-h-04-0-UT.r1 NIH_MGC_36 Homo sapiens CDNA clone
IMAGE:3055710 5', mRNA sequence.
ACCESSION AW403220
VERSION AW403220.1 GI:6922096
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://www-bio.llnl.gov/bdrrp/image.html>
Seq primer: M13 Forward.

FEATURES
source

1. 471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3055710"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (RT)"
/clone="NIH-MGC_36"
/note="Vector: p7713-Pec; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and Mary Soares, Ph.D."

BASE COUNT 98 a 127 c 143 g 103 t

ORIGIN

Query Match 68.2%; Score 268.2; DB 9; Length 471;
 Best Local Similarity 93.9%; Pred. No. 2.5e-63;
 Matches 279; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 83
 |||||||
 DB 87 GGTGAGTCTGGGGAGGCGCTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 146
 |||||||

QY 84 CTCGTGATTCACCTTCACTAGCTATAGCATGCATGGTCCGCCAGGGTCCAGGAAAGG 143
 |||||||
 DB 147 CTCGTGATTCACCTTCACTAGCTATAGCATGCATGGTCCGCCAGGGTCCAGGAAAGG 206
 |||||||

QY 144 GCTGAGTGGGTCTCATCTCATTAATAGTAATATACATATACATGAGAGAGCGAGT 203
 |||||||
 DB 207 GCTGAGTGGGTCTCATCTCATTAATAGTAATAGTAATGTTTCTCATATCTAGAGACTCAGT 266
 |||||||

QY 204 GAAGGGCCGATTTCACATCTCCAGAGACAGCCAGAACTCAGTATCTGCAATGAA 263
 |||||||
 DB 267 GAAGGGCCGATTTCACATCTCCAGAGACAGCCAGAACTCAGTATCTGCAATGAA 326
 |||||||

QY 264 CAGCTTGAGAGCCGAGCAGCAGCGCTGTACTACTGTCCGAGAGATTCTAGATACAG 320
 |||||||
 DB 327 CAGCTTGAGAGCCGAGCAGCAGCGCTGTACTACTGTCCGAGAGATTCTAGATACAG 383
 |||||||

RESULT 11

LOCUS BG686881 908 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602650867F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763153 5',
 mRNA sequence.
 ACCESSION BG686881
 VERSION BG686881.1 GI:13918278
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 908)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabp@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNCM1618 row: f column: 18
 High quality sequence stop: 899.
 Location/Qualifiers
 1..908
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4763153"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."
 BASE COUNT 200 a 262 c 250 g 194 t 2 others

ORIGIN

Query Match 68.2%; Score 268.2; DB 10; Length 908;
 Best Local Similarity 96.8%; Pred. No. 3.7e-63;
 Matches 273; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 83
 |||||||
 DB 139 GGTGAGTCTGGGGAGGCGCTGTCAGACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 198
 |||||||

QY 84 CTCGTGATTCACCTTCACTAGCTATAGCATGCATGGTCCGCCAGGGTCCAGGAAAGG 143
 |||||||
 DB 199 CTCGTGATTCACCTTCACTAGCTATAGCATGCATGGTCCGCCAGGGTCCAGGAAAGG 258
 |||||||

QY 144 GCTGAGTGGGTCTCATCTCATTAATAGTAATATACATATACATGAGAGAGCGAGT 203
 |||||||
 DB 259 GCTGAGTGGGTCTCATCTCATTAATAGTAATAGTAATGTTTCTCATATCTAGAGACTCAGT 318
 |||||||

QY 204 GAAGGGCCGATTTCACATCTCCAGAGACAGCCAGAACTCAGTATCTGCAATGAA 263
 |||||||
 DB 319 GAAGGGCCGATTTCACATCTCCAGAGACAGCCAGAACTCAGTATCTGCAATGAA 378
 |||||||

QY 264 CAGCTTGAGAGCCGAGCAGCAGCGCTGTACTACTGTCCGAG 305
 |||||||
 DB 379 CAGCTTGAGAGCCGAGCAGCAGCGCTGTACTACTGTCCGAG 420
 |||||||

RESULT 12

LOCUS AM403886 397 bp mRNA linear EST 16-FEB-2000
 DEFINITION UI-HF-BK0-abo-d-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3057064 5', mRNA sequence.
 ACCESSION AM403886
 VERSION AM403886.1 GI:6923039
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 397)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabp@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov/db/ftp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
 1..397
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057064"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /clone_lib="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_36"
 /note="Vector: pRT73-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 87 a 92 c 120 g 98 t

Query Match 68.0%; Score 267.4; DB 9; Length 397;
 Best Local Similarity 93.0%; Pred. No. 3.9e-63;
 Matches 280; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGAGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAC 83
 DB 88 GGTGAGTCTGGGGAGAGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAC 147
 QY 84 CTCTGATTACCTTCAGTAGTACTATAGACATGACATGCTGGCCGCAAGGGTCCAGGAAAGG 143
 DB 148 CTCTGATTACCTTCAGTAGTACTATAGACATGACATGCTGGCCGCAAGGGTCCAGGAAAGG 207
 QY 144 GCTGAGTGGTCTCATCTCATCTAGTAAATAGTAACTACTATCTACGACAGCAGT 203
 DB 208 GCTGAGTGGTCTCATCTCATCTAGTAAATAGTAACTACTATCTACGACAGCAGT 267
 QY 204 GAAGGCGGATTCACATCTCCAGAGACAGCCCAAGAACTCATCTATCTCAATGAA 263
 DB 268 GAAGGCGGATTCACATCTCCAGAGACAGCCCAAGAACTCATCTATCTCAATGAA 327
 QY 264 CAGCCTGAGAGCCGAGACAGCGCTGTGTACTACTGTGGAGAGATTTAGTATAGTAA 323
 DB 328 CAGCCTGAGAGCCGAGACAGCGCTGTGTACTACTGTGGAGAGATTTAGTATAGTAA 387
 QY 324 T 324
 DB 388 T 388

RESULT 13
 LOCUS BX379829 1138 bp mRNA linear EST 08-MAY-2003
 DEFINITION BX379829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1040YE16 5-PRIME, mRNA sequence.
 ACCESSION BX379829
 VERSION BX379829.1 GI:30454789
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1138)
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7198.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1040BC08QPl&cluster=7198.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0D1040BC08QPl.
 Location/Qualifiers
 1..1138
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1040YE16"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and EcoRV into the NotI and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 250 a 323 c 329 g 225 t
 ORIGIN
 Query Match 67.9%; Score 266.8; DB 13; Length 1138;

Best Local Similarity 86.5%; Pred. No. 1e-62;
 Matches 320; Conservative 0; Mismatches 17; Indels 33; Gaps 1;

QY 24 GGTGAGTCTGGGGAGAGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAC 83
 DB 197 GGTGAGTCTGGGGAGAGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAC 236
 QY 84 CTCTGATTACCTTCAGTAGTACTATAGACATGACATGCTGGCCGCAAGGGTCCAGGAAAGG 143
 DB 257 CTCTGATTACCTTCAGTAGTACTATAGACATGACATGCTGGCCGCAAGGGTCCAGGAAAGG 316
 QY 144 GCTGAGTGGTCTCATCTCATCTAGTAAATAGTAACTACTATCTACGACAGCAGT 203
 DB 317 GCTGAGTGGTCTCATCTCATCTAGTAAATAGTAACTACTATCTACGACAGCAGT 376
 QY 204 GAAGGCGGATTCACATCTCCAGAGACAGCCCAAGAACTCATCTATCTCAATGAA 263
 DB 377 GAAGGCGGATTCACATCTCCAGAGACAGCCCAAGAACTCATCTATCTCAATGAA 436
 QY 264 CAGCCTGAGAGCCGAGACAGCGCTGTGTACTACTGTGGAGAGATTTAGTATAGTAA 323
 DB 437 CAGCCTGAGAGCCGAGACAGCGCTGTGTACTACTGTGGAGAGATTTAGTATAGTAA 480
 QY 324 TTTCCTCCGTTGGTGGAGCGAGCTATGAGCTGTGGGGCCAGAGGACACGGTCAT 383
 DB 481 -----GGGGTACGGATGAGACTGTGGGGCCAGAGGACACGGTCAC 523
 QY 384 GGTCTCTCA 393
 DB 524 GGTCTCTCA 533

RESULT 14
 LOCUS BX417408 1201 bp mRNA linear EST 13-MAY-2003
 DEFINITION BX417408 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009Y115
 5-PRIME, mRNA sequence.
 ACCESSION BX417408
 VERSION BX417408.1 GI:30650401
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7198.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DE009AE08QPl&cluster=7198.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DE009AE08QPl.
 Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE009Y115"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with NotI and EcoRV
 sites of the pCMVSPORT 6 vector.
 Library was not normalized."

following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.

BASE COUNT 156 a 207 c 213 g 161 t 1 others

Query Match 67.0%; Score 263.2; DB 10; Length 738;
Best Local Similarity 96.9%; Pred. No. 7.8e-62; Indels 1; Gaps 1;
Matches 279; Conservative 0; Mismatches 8;

24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCTGGGGGGTCCCTGTGACATCTCTGTGCAGC 83
134 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCTGGGGGGTCCCTGTGACATCTCTGTGCAGC 193
84 CTCTGATTCACCTTCAGTACCTATAGCATGCACTGGTCCGCCAGGTCGAGGAAAGG 143
194 CTCTGATTCACCTTCAGTACCTATAGCATGCACTGGTCCGCCAGGTCGAGGAAAGG 252
144 GCTGAGTGGGTCTCATTCATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 203
253 GCTGAGTGGGTCTCATTCATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 312
204 GAAGGGCCGATTCACCATTCGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 263
313 GAAGGGCCGATTCACCATTCGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 372
264 CAGCCTGAGAGCCGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGATTC 311
372 CAGCCTGAGAGCCGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGATTC 420

RESULT 17
BM007475 613 bp mRNA linear EST 30-OCT-2001
LOCUS 603616742F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440475 5',
DEFINITION mRNA sequence.
ACCESSION BM007475
VERSION BM007475.1 GI:16521829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 613)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Mammalian Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcrabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1913 row: d column: 12
High quality sequence stop: 608.
Location/Qualifiers
1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5440475"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the

FEATURES

SOURCE

1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5440475"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 126 a 172 c 174 g 141 t

Query Match 65.8%; Score 258.4; DB 12; Length 613;
Best Local Similarity 94.4%; Pred. No. 1.5e-60; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 16;

24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCTGGGGGGTCCCTGTGACATCTCTGTGCAGC 83
132 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCTGGGGGGTCCCTGTGACATCTCTGTGCAGC 191
84 CTCTGATTCACCTTCAGTACCTATAGCATGCACTGGTCCGCCAGGTCGAGGAAAGG 143
192 CTCTGATTCACCTTCAGTACCTATAGCATGCACTGGTCCGCCAGGTCGAGGAAAGG 251
144 GCTGAGTGGGTCTCATTCATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 203
252 GCTGAGTGGGTCTCATTCATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 311
204 GAAGGGCCGATTCACCATTCGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 263
312 GAAGGGCCGATTCACCATTCGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 371
264 CAGCCTGAGAGCCGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGATTC 307
372 CAGCCTGAGAGCCGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGATTC 415

RESULT 18
BG759748 879 bp mRNA linear EST 15-MAY-2001
LOCUS 602711146F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851587 5',
DEFINITION mRNA sequence.
ACCESSION BG759748
VERSION BG759748.1 GI:14070401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Mammalian Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcrabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1694 row: k column: 12
High quality sequence stop: 879.
Location/Qualifiers
1..879
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851587"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling

FEATURES

SOURCE

1..879
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851587"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library.¹⁰

ORIGIN

Query Match	65.5%	Score 257.4	DB 13	Length 890
Best Local Similarity	92.8%	Pred. No. 3.4e-60		
Matches 270	Conservative	0	Mismatches 21	Indels 0
				Gaps 0

Db	129	GGTGGATTCGTGGGGGAGGCGCTGGTCAAGCCGTGGGGGGGTCCCTGAGACTCTCTGTGCAGC	188
QY	84	CTCTGGATTACCTTCCAGTACGTATAGACATCACTGGGTCCGCCAGGSTCCAGGGAAGG	143
Db	189	CTCTGGATTCCCCCTACAGTAGTATTACCATGAACCTGGGTCCGCCAGGCTCCAGGGAAAGG	248
QY	144	GCTGGAGTGGGTCATCATTCATTAGTAATAGTAATCTACATATCTACGACAGCACTAGT	203
Db	249	GCTAGATTGGGTCATCATTCATTAGTGGTGGTACTAGTACTAGTACTATACATACGACAGCACTAGT	308
QY	204	GAAGGCGCATTCACCATCTTCACAGACAAACGCCAAGAATCTACTGTATCTGCAAAATGAA	263
Db	309	GAAGGCGCGATTCCACCATCTTCACAGACAAACGCCAAGAATCTACTGTATCTGCAAAATGAA	368
QY	264	CAGGCTAGAGCCGAGACACAGCGGTGGTACTACGTCGCGAGAGTTGTAG	314
Db	369	CAGCCTAGAGACCCGAGACACAGCGGTGTCTATTACTGTGCGAGAGATGGGAG	419

AM401428	443 bp	mRNA	linear	EST 16-FEB-2000
LOCUS				
DEFINITION	UT-HF-BK0-aad-b-02-0-UT.r1	NT_H_MGC_36	Homo sapiens	cDNA clone
IMAGE:	3053139	5'		mRNA sequence.
ACCESSION	AM401428			
VERSION	AM401428.1	GI:6920011		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 443)			
AUTHORS	NT_H_MGC	http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D.			
	Email: cgapds@email.nih.gov			

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/organism="Homo sapiens"  
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:3053139"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MG685"
/lab_host="DH10B (LTR)"
/clone_lib="NH, MG6, 36"
/notes="vector: p773-Pac; Site_1: NotI; Site_2: Eco RI;
constructed from site fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by
U. Staudt, Ph.D. Library preparation by Maria de Fatima

```

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	Bonaldo, Ph.D. and M. Bento Soares, Ph.D.			
BASE COUNT	93 a	116 c	131 g	103 t
ORIGIN				

Query Match	65.3%;	Score 256.8;	DB 9;	Length 443;
Best Local Similarity	94.0%;	Pred. No. 3.4e-60;		
Matches 267;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;

[illegible]

Search completed: September 24, 2003, 04:42:48
Job time : 2285 secs

Db 61 TCCCTGAGACTCTCTCTGTCAGCCCTCTGATTCACCTTCAGTAGCTATAGCATGCACTGG 120
QY 121 GTCCGCCAGAGGTCACAGGGAAGGGGCTGAGTGGGTCTCATTCATTAGTAATAGTAATCT 180
Db 121 GTCCGCCAGAGGTCACAGGGAAGGGGCTGAGTGGGTCTCATTCATTAGTAATAGTAATCT 180
QY 181 TACATATCTAGCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 240
Db 181 TACATATCTAGCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 240
QY 241 AACTCAGTCTATCTGCAATGAACAGCCCTGAGAGCCGACACAGCGCTGTGTACTACTGT 300
Db 241 AACTCAGTCTATCTGCAATGAACAGCCCTGAGAGCCGACACAGCGCTGTGTACTACTGT 300
QY 301 GGAGAGATTCTAGATAGACGTAATTTCTCGTGGTTCGGAGGAGGAGGATGAGAGCTC 360
Db 301 GGAGAGATTCTAGATAGACGTAATTTCTCGTGGTTCGGAGGAGGAGGATGAGAGCTC 360
QY 361 TGGGGCCAGAGGACGACGCTCATCGTCTCTCA 393
Db 361 TGGGGCCAGAGGACGACGCTCATCGTCTCTCA 393

RESULT 2
US-09-240-274-96
Sequence 96, Application US/09240274
Patent No. 6253455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 96
LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E01
US-09-240-274-96

Query Match 92.5%; Score 363.6; DB 3; Length 381;
Best Local Similarity 98.9%; Pred. No. 8.4e-104;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 24 GGTGAGTCTGGGGAGGCGCTGCAAGCTGGGGGGCCCGAGACGCTCTCTGTCAGC 83
Db 12 GGTGAGTCTGGGGAGGCGCTGTCAGCCTGGGGGGCTCTGTCAGCCTCTCTGTCAGC 71
QY 84 CTCTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
Db 72 CTCTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 131
QY 144 GCTGAGTGGTCTCATCCATTAGTAATAGTAATCTTACATATATCTAGCAGCAGT 203
Db 132 GCTGAGTGGTCTCATCCATTAGTAATAGTAATCTTACATATATCTAGCAGCAGT 191
QY 204 GAAGGCGGATTCACCATCTCCAGAGAACGCCAAGAACTCACTACTGTCTGCAAAATGA 263
Db 192 GAAGGCGGATTCACCATCTCCAGAGAACGCCAAGAACTCACTACTGTCTGCAAAATGA 251
QY 264 CAGCTGAGAGCGGAGACAGCGCTGTACTACTGTGAGAGATTTAGATACAGTAA 323
Db 252 CAGCTGAGAGCGGAGACAGCGCTGTACTACTGTGAGAGATTTAGATACAGTAA 311
QY 324 TTTCCTCGGTTGGTTCGGAGGAGCGATATGAGCTGTGGGGCCAAAGGACACAGCTCAT 383

Db 312 TTTCTCTCGTGGGTTCGGAGCGGATGAGACGCTCTGGGGCCAAAGGACACAGCTCAT 371
QY 384 CGTCTCTCA 393
Db 372 CGTCTCTCA 381

RESULT 3
US-08-545-809A-21
Sequence 21, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
US-08-545-809A-21

Query Match 69.3%; Score 272.2; DB 3; Length 519;
Best Local Similarity 97.2%; Pred. No. 2.6e-75;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGCCTGGGGGGTCCCTAGACCTCTCTGTCAGC 83
Db 180 GGTGAGTCTGGGGAGGCGCTGTCAGCCTGGGGGGTCCCTAGACCTCTCTGTCAGC 239
QY 84 CTCTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
Db 240 CTCTGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 299
QY 144 GCTGAGTGGTCTCATCCATTAGTAATAGTAATCTTACATATATCTAGCAGCAGT 203
Db 300 GCTGAGTGGTCTCATCCATTAGTAATAGTAATCTTACATATATCTAGCAGCAGT 359

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Db	244	CAAAATACAGCCTGAGACCCGAGACACGGCTGTTATTATCTGTGGAAAG-----TA	297
QY	316	TACAGTAATTTCTCCGTTGGTTGCGACACGTTATGACGCTGTGGGCCAAGGACC	375
Db	298	TTATATTTTGACATCAAAACAACCTTTATTACTACTACATGACGCTGTGGGCCAAAGGACC	357
QY	376	ACGGTCATCGTCTCTCA	393
Db	358	ACGGTCGCCGCTCTCTCA	375

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RESULT 6
US-10-039-785-65
Sequence 65, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIORITY APPLICATION NUMBER: 60/369,860
PRIORITY FILING DATE: 2002-04-05
PRIORITY APPLICATION NUMBER: 60/341,237
PRIORITY FILING DATE: 2001-12-20
PRIORITY APPLICATION NUMBER: 60/331,110
PRIORITY FILING DATE: 2001-11-14
PRIORITY APPLICATION NUMBER: 60/331,044
PRIORITY FILING DATE: 2001-11-07
PRIORITY APPLICATION NUMBER: 60/327,364
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/323,807
PRIORITY FILING DATE: 2001-09-21
PRIORITY APPLICATION NUMBER: 60/309,176
PRIORITY FILING DATE: 2001-08-02
PRIORITY APPLICATION NUMBER: 60/294,981
PRIORITY FILING DATE: 2001-06-04
PRIORITY APPLICATION NUMBER: 60/293,473
PRIORITY FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 747
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65

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Query Match	63.1%;	Score 248;	DB 4;	Length 747;
Best Local Similarity	82.0%;	Pred. No. 1e-67;		
Matches 300;	Conservative	0;	Mismatches 60;	Indels 6;
				Gaps 1;

QY 2 GGGAGAGTGTGGGGGGGGCGTCAACCGGGGGGGCCCTGAGACTCTCCGTGACG 83
 Db 12 GTTGGAGTGTGGGGGAGGCTTGTGTAACGCTGGGGGGTCCCTGAGACTCTCTGTGACG 71
 QY 84 CTCTGGATTACCTTCAGTAGTATATAGCATGCACCTGGGTCCGCGAGGGTCCAGGAGGG 143
 Db 72 CTCTGGATTACCTTCAGTAGTATATAGCATGCACCTGGGTCCGCGAGGGTCCAGGAGGG 131
 QY 144 GGTGAGTGTGGTCTATCATCTAGTAATAAGTAATACTTACATATACGCACAACGACG 203
 Db 132 GCTGGAGTGTGGTCTCAGCTATTAGTGGTGAAGTGGTGAAGCACAATACTACGACGATCCGG 191
 QY 204 GAAGGGCGCATTCACCATCTCCAGGAAACAAGCCCAAGACCTGTAATTCGAATATGAA 263
 Db 192 GAAGGGCGGTTCCACCATCTCCAGGAAACAATTCGAAGACACGGTGTATTCGAATATGAA 251
 QY 264 CAGCTGAGAGCCGAGCACACGGCTGTGTACTACTGTGCGAGAGATTCTATGATATACGTA 323

Db	252	CACCTGAGAGCCGAGAGACACGCCGTGATTACTGTCGAGAGAACCATCTTTCAGCA	311
QY	324	TTCCTCCTCGTTGGGTTCCGAGGACGGATATGAGCTGGGGCCCAAGGACACAGGCAT	383
Db	312	GTCGGGCGCACT-----ACTCCTACGGTGATGAGACTCTCTGGGGCCAGAGCAATAGTCAC	365
QY	384	CGTCTC	389
Db	366	CGTCTC	371

RESULT 7
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 : Sequence 11, Application US/08545809A
 : Patent No. 6096878
 :
 : GENERAL INFORMATION:
 : APPLICANT: Honjo, Tasuku
 : APPLICANT: Matsuda, Fumihiko
 : TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
 : NUMBER OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 : NUMBER OF SEQUENCES: 145
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Fish & Richardson, P.C.
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: US
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows95
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/545, 809A
 : FILING DATE: 27-MAR-1996
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/JP93/00603
 : FILING DATE: 10-MAY-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Freeman, John W.
 : REGISTRATION NUMBER: 29,066
 : REFERENCE/DOCKET NUMBER: 06501/004001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-542-5070
 : TELEFAX: 617-542-8906
 : TELEX: 200154
 : INFORMATION FOR SEQ ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 715 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: Genomic DNA
 : ORIGINAL SOURCE:
 : ORGANISM: Homo sapiens
 : CELL TYPE: human lymphoblast
 : CELL LINE: CGM1
 : US-08-545-809A-11

Query Match	62.5%	Score 245.8;	DB 3;	Length 715;
Best Local Similarity	87.9%;	Pred. No. 4.8e-67;		
Matches 268; Conservative	0;	Mismatches 37;	Indels 0;	Gaps 0;

[illegible]

D _b	471	CGCCAGGCTCCAGGGGAAGGGGTGGAGTGGTTTCATACATTAGTAGTGSTAGTACC	530
O _Y	184	ATATPCTHCGCAGACGCAGTGAAGGGCCGATTCCACATFTCCAGAGAACAACGCCAAGAAC	243
D _b	531	ATATPCTHCGCAGACTCTGTGAAGGGCCGATTCCACATFTCCAGGGACAACGCCAAGAAC	590
O _Y	244	TCACGTATHTGCAATATGAACAGCTGAGAGCCGAGCACACGGCTGTGTACTACTGTGCG	303
D _b	591	TCACGTATHTGCAATATGAACAGCTGAGAGCCGAGCACACGGCTGTATTACTGTGCG	650
O _Y	304	AGAGA	308
D _b	651	AGAGA	655

```

: RESULT 8
: US-09-240-274-182
: Sequence 182, Application US/09240274
: Patent No. 6253455
: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 182
: LENGTH: 381
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) antibody clone SH10
: US-09-240-274-182

```

Query Match	62.1%;	Score 244.2;	DB 3;	Length 381;
Best Local Similarity	80.8%;	Pred. No. 1,2e-66;		
Matches 298;	Conservative	0;	Mismatches 68;	Indels 3;
			Gaps	1
QY	GTGGAGTGTGGGGGAGGCGCTGTCAAGCGCTGGGGGGTCCCTGAGACTCCTCGTGCAGCC	84		
Db	GAGAGTGTGGGGGAGGCGGTGTCCAGCGCTGGGAGGTCCCTGAGACTCCTCGTGCAGCG	75		
QY	85 TCTGGAATTCACCTTCAGTAGCTATAGCATGACACTGGGTCCGCCAAGGTCCAGGAAGGG	144		
Db	76 TCTGGGTTCACCTTCAGTAGGAATGGCATGCACTGGGTCCGCCAAGGTCTGGCAAGGG	135		
QY	145 CTGGAGTGGGTCTCATCCATTAGTATAGTATATCTACTCATATCTACGAGAGCCAGT	204		
Db	136 CTGGAGTGGGTGGCGCTTTATATAGTTTATGGAATATATTAATCTATGACAGCTCCGG	195		
QY	205 AAGGCGCATTCACCATTCCACAGAGACACGCAAGCAACTCACTATCTGCAAAATGAAC	264		
Db	196 AAGGCGCATTCACCATTCCACAGAGACAAATTCGAAGAACAGCTGTATCTGCAAAATGAAC	255		
QY	265 AGCTGAGAGCCGAGACACAGCGCTGTGTACTACTCTGCGAGAGATTTAGATACAGTANT	324		
Db	256 AGCTGGAAGCGGAGACACAGCGCTGTGTAATTACTGTGGAGAGAGAGAGGCTGTGTTTCGG	315		
QY	325 TTCTCCGCTTGTGGGAGGAGCGGTATGACGCTGCGGGCGAAGGGACCGGCTATC	384		
Db	316 GGACTTAATCGG---TGSTCTACAGGCAATGACGCTGTGGGGCAAGGACCAAGGTCAAGC	372		
QY	385 GTCTCTCTCA	393		
Db	373 GTCTCTCTCA	381		

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: RESULT 9
: US-09-240-274-195
: Sequence 195, Application US/09240274
: Patent No. 6253455
: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 195
: LENGTH: 378
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) antibody clone SH54
: US-09-240-274-195

```

	Query Match	62.0%:	Score 243.6:	DB 3:	Length 378:
	Best Local Similarity	80.5%:	Pred. No. 1.8e-66:		
	Matches	Conservative	0:	Mismatches 69:	Indels 3: Gaps 1
OY	24	GATGAGTCTGGGGGAGCGCTGTGCACCCCTGGGGGGTCCTGGAACACTCCTCTGCAAGC	83		
Dd	12	GCTCGAGTCGGGGGGAGCGCTGTGCACCCCTGGGAGGTCCCTGNAACACTCCTCTGTGCAAGC	71		
OY	84	CTTGAGATTACCTTCAGTAGCTATATGATGCATGCATCTGGTCCGCCAGGCTCCAGSAAAGG	143		
Dd	72	-GTCTGGGTTACCTTCAGTAGGAATGAGCATGCATGCGGTCCGCCAGGCTCCGCCAAGAAGG	131		
OY	144	GCTGAGTGGGGTCTCCATTCAGTAAGTAAGTAATTCATAATATCTACGCAAGACAGT	203		
Dd	132	GCTGAGTGGGGGCTATTTATATATGTTTGAATGAGAGTAATTAATTAATGACAGACTCCGT	191		
OY	204	GAAGGGCCGATTACACATCTCCAGAGACAGCCCAAGAACTCACTGTATCTGCAATGAA	263		
Dd	192	GAAGGGCCGATTACACATCTCCAGAGACAATTCGAAGAACAACGGTGTATCTGCAATGAA	251		
OY	264	CAGCTGAGAGCCGAGCACAGGCGTGTACTACTCTGTCCGAGAGATTCTAGATACAGTRA	323		
Dd	252	CAGCCTGAGACCAGCAGACAGGCGTGTATTATTAAGTCCGGAAGAGGAGGCTCTGTTTCG	311		
OY	324	TTCCTCGTTGGGTTGGAGAGAGCGATATGAGACTCTGGGGCCCAAGSAGACAGGTAT	383		
Dd	312	GGGAACTTACTCG---TGCTCTACGGTATATGACACTCTGGGCCCAAGSGAACACAGCTCAG	368		
OY	384	CGTCTCTCA	393		
Dd	369	CGTCTCTCA	378		

```

RESULT 10
US-09-240-274-95
; Sequence 95, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLED
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081, 380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028, 550

```

EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 95
LENGTH: 378
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

Query Match 61.6%; Score 242; DB 3; Length 378;
Best Local Similarity 80.3%; Pred. No. 5.7e-66;
Matches 297; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

OY 24 GGTGAGTCTGGGGAGGCGCTGATCAAGCCTGGGGGTCCTGAGACTCTCTGTCAGC 83
DB 12 GCTCGAGTCTGGGGAGGCGCTGATCAAGCCTGGGGGTCCTGAGACTCTCTGTCAGC 71
OY 84 CTCTGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 143
DB 72 GTCTGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 131
OY 144 GCTGAGTGGTCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 203
DB 132 GCTGAGTGGTCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 191
OY 204 GAAGGGCGGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 263
DB 192 GAAGGGCGGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 251
OY 264 CAGCTGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 323
DB 252 CAGCTGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308
OY 324 TTCTCTCGTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383
DB 309 GAGTGTGATTCCTCCCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 368
OY 384 CGTCTCTCA 393
DB 369 CGTCTCTCA 378

RESULT 11
US-08-082-623-1
Sequence 1, Application US/08082623
Patent No. 5750106
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,623
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,228
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-055-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..369
OTHER INFORMATION: /standard_name="Nucleotide"
OTHER INFORMATION: Sequence of the V-h region of SDZ MSL 109"
Patent No. 5750106
US-08-082-623-1

Query Match 61.2%; Score 240.4; DB 1; Length 369;
Best Local Similarity 80.9%; Pred. No. 1.8e-65;
Matches 296; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

OY 16 GAGTCTGGGAGTCTGGGGAGGCGCTGATCAAGCCTGGGGGTCCTGAGACTCTGC 75
DB 4 GAGCAAGTGTGATCTGGGGAGGCGCTGATCAAGCCTGGGGGTCCTGAGACTCTGC 63
OY 76 TGTGAGCCTCTGGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 135
DB 64 TGTGAGCCTCTGGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 123
OY 136 GGAAGGGGCTGAGTGGGTCATCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 195
DB 124 GGAAGGGGCTGAGTGGGTCATCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 183
OY 196 GAGCGAGTGAAGGCGATTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 255
DB 184 GAGTGTGAGGAGGCGCTTCACCTTCAGTAGTATATGATGATGATGATGATGATGATGATGATGATGAT 243
OY 256 CAATGAGAGCCTGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315
DB 244 CAATGAGAGCCTGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
OY 316 TACAGTAATTTCTCTCCGT-----TGGTTGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 363
DB 304 TATTACGCTTTTCAGAGTGGTCTTTGTGAGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 363
OY 367 CAAGGG 372
DB 364 CAAGGG 369

RESULT 12
US-09-240-274-94
Sequence 94, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 94
;
; LENGTH: 378
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

```

Query Match	60.8%;	Score 238.8;	DB 3;	Length 378;
Best Local Similarity	79.7%;	Pred. No. 5.6e-65;		
Matches 295;	Conservative 0;	Mismatches 72;	Indels 3;	Gaps 1;

Oy	24	GGTGGAGCTCTGGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCGAGACCTCTCCGTGTGCAC	83
Db	12	GCTCGAGTCGGGGGGAGGCGTGGTCCAGCTCTGGGAGGTCCCTGGAGCTCTCTGTGTGCAC	71
Oy	84	CTCTGGATTACCTTCAGTACGTATGAGCATGCACAGGGGTCCGCCAGGGGTCCAGGGAAGGG	143
Db	72	GCTCGGATTTCACCTTCAGTACGTATGAGCATGCACAGGGGTCCGCCAGGGGTCCAGGGAAGGG	131
Oy	144	GCTGGAGTGGGCTCTCATCCATTAGTAATAGTAATAGTAATCTTACATATATACGACAGCGCAGT	203
Db	132	GCTGGAGTGGGCGAGTTGTCTACTATGATGGAAGTAAACAACACTATTTCAGACTCCGT	191
Oy	204	GAAGGGCCGATTACACATCTCCAGAGACAAAGCCCAAGAACTACTGTATCTGCAATGAA	263
Db	192	GAAGGGCCGATTACACATCTCCAGAGACAAAGCCCAAGAACTACTGTATCTGCAATGAA	251
Oy	264	CAGCCTGAGAGCCGAGCACAGCGCTGTGACTACTAGTGCGAGAGATTTCTAGATTACAGTAA	323
Db	252	CAGCCTGAGAGCCGAGAGCACAGCGCTGTGATTACTGTGCGAGAGA--AAGAAATTTTGG	308
Oy	324	TTTCTCTCCGTTGGGTTTCGGAGCGATGAGAGCTCTGGGGCCAAAGGAGACACGGTCAAT	383
Db	309	GAGTGGTATTTCCTCCCTACTACTAGGATGAGATGACGATCTGGGGCCCAAGGAGACACGGTCAAC	368
Oy	384	CGTCTCTCTCA	393
Db	369	CGTCTCTCTCA	378

RESULT 13
US-09-240-274-196
; Sequence 196, Application US/09240274

```

? GENERAL INFORMATION:
? APPLICANT: Siegel, Donald L.
? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
? FILE REFERENCE: 08596-4202
? CURRENT APPLICATION NUMBER: US/09/240,274
? CURRENT FILING DATE: 1999-01-29
? EARLIER APPLICATION NUMBER: 60/081,380
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/028,550
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 196
? LENGTH: 378
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) antibody clone SH56
? US-09-240-274-196

```

Query Match	60.8%	Score 238.8	DB 3	Length 378:
Similarity	79.7%	Pred. No.5.6e-65;		
Match	Conservative	0	Mismatches 72;	Indels 3; Gaps 1.
24	GGTGAGTCTCTGGGGAGGCGCTGCTCAAGCCCTGGGGGGGTCCTGAGACATCTCTGTGGAGC	83		
Db	12 GCTGAGATCGGGGGAGGCGCTGCTCAAGCCCTGGGGGGGTCCTGAGACATCTCTGTGGAGC	71		

QY	84	CTCTGATTCACCTTCAGTAGCTATATAGCATATGCACCTGGTCCGCGAAGGTCCAGGAAAGG	143
Db	72	GCTCGATTCCACCTTCAGTAGCTATATGCATATGCACCTGGTCCGCGAAGGTCCAGGAAAGG	121
QY	144	GCTGGAGTGGGTCTATCATCTAGTAAATAGTAATACTTACATATCTACTACGCAACCCACT	203
Db	132	GCTGGAGTGGGTGGGACATTTCTACTATATGAAATTAACAAACACTATTCAACCTCCGT	191
QY	204	GAAAGGCCGATTCACCATCTCCAGAGACAAGCAGCAAGAACTCACTATATCGAAATGAA	263
Db	192	GAAAGGCCGATTCACCATCTTCAGAGACAACCTCCAAAGAACAGCGTGTATCTACAAATGGA	251
QY	264	CAGCCTGAGAGCCGAGACACAGCGCTGTGTACTACTGTGCGAGAGATTCAGATTAACGTAA	323
Db	252	CAGCCTGAGAGCCGAGAGACACAGCGCTGTGTATTACTGTGGAGAGA--AAGAAATTTTCG	308
QY	324	TTTCCCTCCGTTGGGTTCCGAGCGACGCTATGACGCTGTGGGCCCAAGGACACCGGTCAAT	383
Db	309	GAGTGGTTATTTCCCGCTACTACTACAGGTATGACGCTGTGGGCCCAAGGACACCGGTCAAC	368
QY	384	CGCTCCATCA	393
Db	369	CGCTCCATCA	378

```

RESULT 14
US-09-560-198A-1
; Sequence 1, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peter SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific blinding members for TGPetrol
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ. ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO. 1
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-560-198A-1

```

Query Match	60.3%	Score 236.8;	DB 4;	Length 369;
Best Local Similarity	80.0%	Pred. No. 2.3e-64;		
Matches 296; Conservative	0;	Mismatches 62;	Indels 12;	Gaps 1;

QY	24	GGTGTGAGCTGTGGGGGAGGCGCTGTGTAAGCTGTGGGGGTCCGTGAGACTCTCCTGTGCAGC	83
Db	12	GGTGAAGTCTGTGGGGGAGGCGTGTGATCAGGCTGTGGAGGTCCCTGTGAGACTCTCCTGTGCAGC	71
QY	84	CTCTGGAAATTCACCTTTCAGTAGCATATAGCATGTCAGTGGTCCGCGCAGAGGTCACGAGGAAGG	143
Db	72	CTCTGGATTCACCTTTCAGTAGCATATAGCATGTCAGTGGTCCGCGCAGAGGTCACGAGGAAGG	131
QY	144	GCTGGAGTGGGTCTCATTCATTAGTAATAGTAATCTTACATATTAATCTATACGCAGACGCAGT	203
Db	132	GCTGGAGTGGGTGGTGGCAGTATATCATATGATGTGAGACTATTAATTAATCTATGCAGACCTCGT	191
QY	204	GAGGGCCGATTCCACCATCTCCAGAGACAAGCCCAAGAACTCACTGTATCTGCAATGAA	26
Db	192	GAGGGCCGATTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAA	251

QY	264	CAAGCTGAGAGCCGACACACGGGCTGTCTACTACGTGGCCGAGATATCTGTGATACACTAA	333
Db	252	CACCGCTGAGAGCGCTGAGACACACGGCTGTGTATTACTGTGCGGAACCTGATATATATGCG	311
QY	324	TTTCTCCCTTGGGTTTCGAGACGACGATATGAGCTCTGGGGCCAAAGGACACACGGTCAT	383
Db	312	CTAC-----GATACGAGTGTGTGTGAGCTCTGGGGGCCAAGGACACACGGTCAC	359
QY	384	CGTCTCTCTCA	393
Db	360	CGTCTCTCTCA	369

Query	Match	Best Local Similarity	Matches	Score	DB	Length	939:
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	GENERAL INFORMATION:	59.9%;	235.6;	DB 4;	Length 939;
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	APPLICANT: Adams, Camilla W.	80.1%;	Pred. No. 8e-64;		
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	APPLICANT: Ashkenazi, Avi J.	0;	Mismatches 64;	Indels 9;	Gaps 1;
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	APPLICANT: Chutkenarai, Anan				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	APPLICANT: Kim, Kyung J.				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TITLE OF INVENTION: Apo-2 Receptor				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	NUMBER OF SEQUENCES: 14				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	CORRESPONDENCE ADDRESS:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	ADDRESSEE: Genentech, Inc.				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	STREET: 1 DNA Way				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	CITY: South San Francisco				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	STATE: California				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	COUNTRY: USA				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	ZIP: 94080				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	COMPUTER READABLE FORM:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	COMPUTER: IBM PC compatible				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	OPERATING SYSTEM: PC-DOS/MS-DOS				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	SOFTWARE: WinPatIn (Genentech)				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	CURRENT APPLICATION DATA:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	APPLICATION NUMBER: US/09/079,029				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	FILING DATE:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	CLASSIFICATION:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	ATTORNEY/AGENT INFORMATION:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	NAME: Marschang, Diane L.				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	REGISTRATION NUMBER: 35,600				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	REFERENCE/DOCKET NUMBER: P1101R2				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TELECOMMUNICATION INFORMATION:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TELEPHONE: 650/952-9881				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TELEFAX: 650/225-5416				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	INFORMATION FOR SEQ ID NO: 7:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	SEQUENCE CHARACTERISTICS:				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	LENGTH: 939 base pairs				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TYPE: Nucleic Acid				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	STRANDEDNESS: Single				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369	TOPOLOGY: Linear				
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369					
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369					
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369					
US-09-079-029-7	Sequence 7, Application us/09079029	Patent No. 6342369					

Db	309	GAAGGCGCATTCACCATCTCCAGAGCAACAGCCCAAGACTCACTGTATCTGCACAAATGAA	368
QY	264	CACCTGAGAGCCGAGACACACAGCGCTGTACTACTGTCGCGAGATCTCTAGATATACAGTA	323
Db	369	CACCTGAGAGCCGAGAGACAGCGCTGTATATTACTGTGCGAGAGATCTTTTAAAGGTCAA	428
QY	324	TTTCTCCCGTTGGGTTCCGAGCAGAGATATGGAGCTGGGGCCAAAGAGACACAGGTCA	383
Db	429	GGCGAGTGTCTCGGGTG-----TTGACCCCTGGGGAGAGAGGACACAGGTCA	479
QY	384	CGTCTC	389
Db	480	CGTCTC	485

RESULT 16
 US-08-652-816A-22
 Sequence 22, Application US/08652816A
 Patent No. 5872215
 GENERAL INFORMATION:
 APPLICANT: Osbourn, JK
 APPLICANT: Allen, DJ
 APPLICANT: McCallately, JG
 TITLE OF INVENTION: Specific binding members, materials and
 TITLE OF INVENTION: methods.
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,816A
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.4
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.8
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 23-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9525004.9
 FILING DATE: 07-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9610824.6
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/02240
 FILING DATE: 02-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/244,597
 FILING DATE: 01-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/33308
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 354 base pairs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2003, 04:04:44; Search time 1825 Seconds
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536.093 Million cell updates/sec

Title: US-09-848-798a-97
Perfect score: 393
Sequence: 1 gaggtcagctgctgagtc.....ccagctcagctcctca 393

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	393	11	US-09-848-798-97
2	363.6	92.5	381	11	US-09-848-798-96
3	272.2	69.3	311	9	US-09-864-761-31233
4	270.8	68.9	379	12	US-10-041-860-55
5	269.6	68.6	348	14	US-10-091-300-23
6	269.6	68.6	348	14	US-10-091-300-27
7	268	68.2	348	14	US-10-091-300-30
8	262.8	66.9	414	12	US-10-323-694-143
9	261.2	66.5	379	12	US-10-041-860-59
10	261.2	66.5	382	12	US-10-041-860-75
11	259.2	66.0	1413	14	US-10-153-382-16
12	258	65.6	379	12	US-10-041-860-67
13	250.4	63.7	520	10	US-09-844-684-10
14	250.4	63.7	520	14	US-10-040-244-10
15	248.8	63.3	375	14	US-10-172-317-1
16	248	63.1	407	11	US-09-918-995-16657

17	248	63.1	747	13	US-10-039-785-65	Sequence 65, Appl
18	247.6	63.0	527	10	US-09-964-824A-583	Sequence 583, App
19	247.6	63.0	527	10	US-09-954-456-1188	Sequence 1188, Ap
20	246.4	62.7	666	11	US-09-972-656-73	Sequence 73, Appl
21	245.6	62.5	4026	12	US-09-949-039-1	Sequence 1, Appl1
22	245.6	62.5	4027	12	US-09-969-748C-1	Sequence 182, App
23	244.2	62.1	381	11	US-09-848-798-182	Sequence 125404,
24	244.2	62.1	739	13	US-10-027-633-125404	Sequence 125405,
25	244.2	62.1	739	13	US-10-027-633-125405	Sequence 195, App
26	243.6	62.0	378	11	US-09-848-798-195	Sequence 31, Appl
27	242	61.6	367	12	US-10-330-613-31	Sequence 31, Appl
28	242	61.6	367	12	US-10-330-530-31	Sequence 95, Appl
29	242	61.6	378	11	US-09-848-798-95	Sequence 14, Appl
30	239.6	61.0	630	10	US-09-844-684-14	Sequence 85, Appl
31	239.6	61.0	630	14	US-10-040-244-14	Sequence 94, Appl
32	239.2	60.9	738	12	US-10-120-414-85	Sequence 196, App
33	238.8	60.8	378	11	US-09-848-798-94	Sequence 25, Appl
34	238.8	60.8	378	11	US-09-848-798-196	Sequence 12, Appl
35	238.4	60.7	1427	13	US-10-066-895-25	Sequence 7, Appl1
36	238	60.6	580	10	US-09-844-684-12	Sequence 12, Appl
37	238	60.6	580	14	US-10-040-244-12	Sequence 7, Appl1
38	237.2	60.4	402	9	US-09-811-737-7	Sequence 24, Appl
39	237.2	60.4	788	9	US-09-811-737-24	Sequence 31, Appl
40	237.2	60.4	1708	10	US-09-859-053-31	Sequence 20, Appl
41	236.8	60.3	369	14	US-10-243-265-1	Sequence 58, Appl
42	236.8	60.3	1427	13	US-10-066-895-20	Sequence 58, Appl
43	236.4	60.2	411	10	US-09-423-800-58	Sequence 58, Appl
44	236.4	60.2	411	12	US-10-337-981-58	Sequence 58, Appl
45	236.4	60.2	411	14	US-10-182-018-58	Sequence 58, Appl
46	236.4	60.2	411	14	US-10-169-003-58	Sequence 7, Appl1
47	235.6	59.9	939	12	US-10-288-917-7	Sequence 7, Appl1
48	235.6	59.9	939	13	US-10-052-798-7	Sequence 35, Appl
49	235.2	59.8	1427	13	US-10-066-895-27	Sequence 3, Appl1
50	234	59.5	1673	10	US-09-859-053-35	Sequence 1, Appl1
51	233.6	59.4	369	14	US-10-243-265-3	Sequence 1, Appl1
52	233.4	59.4	1430	12	US-10-225-108A-1	Sequence 14, Appl
53	233.4	59.4	6284	13	US-10-066-895-14	Sequence 67, Appl
54	233.4	59.4	6284	13	US-10-066-895-14	Sequence 109, App
55	233.2	59.3	672	11	US-09-972-656-67	Sequence 87, Appl
56	233	59.3	1603	9	US-09-822-849A-109	Sequence 88, Appl
57	232.4	59.1	381	11	US-09-848-798-87	Sequence 52, Appl
58	232.4	59.1	381	11	US-09-848-798-88	Sequence 183, App
59	231.6	58.9	393	11	US-09-988-115A-52	
60	231.2	58.8	375	11	US-09-848-798-183	

ALIGNMENTS

RESULT 1
US-09-848-798-97
Sequence 97, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848, 798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240, 274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028, 550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 97
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798-97

Query Match	100.0%	Score 393;	DB 11;	Length 393;
Best Local Similarity	100.0%	Pred. No. 6.2e-121;		
Matches 393;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GAGGTGACACTGCTGGAGCTGAGGTGGGTGGAGTCTGGGGGAGAGCCGTGTCACAACTCGGGGG	60
	1	GAGGTGACACTGCTGGAGCTGAGGTGGGTGGAGTCTGGGGGAGAGCCGTGTCACAACTCGGGGG <td>60</td>	60
Db	1	GAGGTGACACTGCTGGAGCTGAGGTGGGTGGAGTCTGGGGGAGAGCCGTGTCACAACTCGGGGG <td>60</td>	60
QY	61	TGCGTGAAGCTGCTGCTGAGACGCTTCGTGATTCACCTTCAGTACGTATAGATGACTGG	120
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Db	61	TGCGTGAAGCTGCTGCTGAGACGCTTCGTGATTCACCTTCAGTACGTATAGATGACTGG	120
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QY	181	TACATTTACTTACGCAGAGCGAGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCAAG	240
	181	TACATTTACTTACGCAGAGCGAGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCAAG	240
Db	181	TACATTTACTTACGCAGAGCGAGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCAAG	240
QY	241	AACCTCACTGATCTGCAAATGAACGACGCTTGAGAGCCGAGACACAGGCTGTGTACTACTGT	300
	241	AACCTCACTGATCTGCAAATGAACGACGCTTGAGAGCCGAGACACAGGCTGTGTACTACTGT	300
Db	241	AACCTCACTGATCTGCAAATGAACGACGCTTGAGAGCCGAGACACAGGCTGTGTACTACTGT	300
QY	301	GGCAGAGATTTAGATACAGTAAATTTCTCGGTTGGGTTCCGAGCGAGCGATATGAGCGTC	360
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Db	301	GGCAGAGATTTAGATACAGTAAATTTCTCGGTTGGGTTCCGAGCGAGCGATATGAGCGTC	360
QY	361	TGGGGGCAAGGAGCACGCGTCACTGCTCTCTCA	393
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Db	361	TGGGGGCAAGGAGCACGCGTCACTGCTCTCTCA	393

RESULT 2
100-94

US-09-848-758-90
; Sequence 96, Application US/09848798
; Publication No. US20030040605A1

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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

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1 FILE REFERENCE: 09596-4202
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3 CURRENT APPLICATION NUMBER: US/09/848,798
4
5 PRIOR FILING DATE: 2001-05-04
6
7 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
8
9 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
10
11 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
12
13 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
14
15 NUMBER OF SEQ ID NOS: 224
16
17 SOFTWARE: PatentIn Ver. 2.0
18
19 SEQ ID NO 96
20
21 LENGTH: 381
22
23 TYPE: DNA
24
25 ORGANISM: Homo sapiens
26
27 FEATURE:
28
29 OTHER INFORMATION: anti-Rh(D) chain E01
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Query Match	92.58;	Score 363.6;	DB 11;	Length 381;
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Best Local Similarity 98.9%; Pred. No. 4e-111;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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24 GGTGAGCTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTCAGC 83

Db 12 GCTCGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCCTGTGCAGC 71

84 CTCTGGATTCACCTTCAGTAGCATGCACTGGGTCGCCAGGCTCCAGGGAAAGG 143
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 72 CTCTGGATTCACCTTCAGTAGCATGCACTGGGTCGCCAGGCTCCAGGGAAAGG 131
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144 GCTGAGTGGCTTCATTCATTAGTAATAGTAATACCTTACATATTACTACGACAGACGAGT 203

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Qy	204	GAAGGGCCGATTTTACCATCTCCAGTCCAGAGACAAAGCCCAAGAACGTCACGTATTCTGCAAAATGAA	267
Db	192	GAAGGGCCGATTTTACCATCTCCAGAGACAAAGCCCAAGAACGTCACGTATTCTGCAAAATGAA	251
Qy	264	CACCTTGAAGAGCCGAGACACAGCGGTGTACTACTGTGCGAGAGATTTTAAATACAGTAA	327
Db	252	CACCTTGAAGAGCCGAGAGACAGCGGTGTGTACTACTGTGCGAGAGATTTTAAATACAGTAA	311
Qy	324	TTTCTCTCGGTTGGGTTCCGAGGCGACGGTATGAGCTCTGGGGGCCAAGGGACCAACGTCAT	388
Db	312	TTTCTCTCGGTTGGGTTCCGAGGCGACGGTATGAGCTCTGGGGGCCAAGGGACCAACGTCAT	372
Qy	384	CGTCTCTCA	393
Db	372	CGTCTCTCA	381

RESULT 3
US-09-86

; Sequence 31233, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION

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; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GE

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
ORDINATE AND TELEPHONE NUMBER: 010 000 0864 761

;
 ; CURRENT APPLICATION NUMBER: US 03/004,100
 ;
 ; CURRENT FILING DATE: 2001-05-23
 ;
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ;

; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263 5

; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/0066
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/JIS01/00666

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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

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PRIOR APPLICATION NUMBER: PCT/US01/006677
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408

;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29

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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31233

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LENGTH: 311

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AB019439.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
OTHER INFORMATION: EST_HUMAN HIT: AMA03220.1, EVALUOE 0.00e+00
OTHER INFORMATION: NT HIT: L29155.1, EVALUOE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUOE 3.00e-43
US-09-864-761-31233

Query Match 69.3%; Score 272.2; DB 9; Length 311;
Best Local Similarity 97.2%; Pred. No. 1.2e-80;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 83
DB 23 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 82
QY 84 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 143
DB 83 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 142
QY 144 GCTGAGTGGTCTTCATCTCATTTAGTATAGTAACTTACATATACGACGACGAGT 203
DB 143 GCTGAGTGGTCTTCATCTCATTTAGTATAGTAACTTACATATACGACGAGT 202
QY 204 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 263
DB 203 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 262
QY 264 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAGA 308
DB 263 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAGA 307

RESULT 4

US-10-041-860-55
Sequence 55, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041.860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-55

Query Match 68.9%; Score 270.8; DB 12; Length 379;
Best Local Similarity 85.1%; Pred. No. 3.8e-80;
Matches 315; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 71
QY 84 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 143
DB 72 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 131

QY 144 GCTGAGTGGGTCTCATCTCATTTAGTATAGTAACTTACATATACGACGACGAGT 203
DB 132 GCTGAGTGGGTCTCATCTCATTTAGTATAGTAACTTACATATACGACGAGT 191
QY 204 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 263
DB 192 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 251
QY 264 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAGATTCTAGATGAA 323
DB 252 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAGATTCTAGATGAA 308
QY 324 TTTCTCCGTTGGGTTCGAGAGCGATGAGCGCTGGGGCCCAAGGACACGCTCAT 383
DB 309 GTTTGGGGGAATTAATGCGCTGCTTCTACTTTGACTACTGCGGCGAGGACCTGCTAC 368
QY 384 GCTCTCTCA 393
DB 369 GCTCTCTCA 378

RESULT 5

US-10-091-300-23
Sequence 23, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091.300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
LENGTH: 348
TYPE: DNA
ORGANISM: Human
US-10-091-300-23

Query Match 68.6%; Score 269.6; DB 14; Length 348;
Best Local Similarity 96.8%; Pred. No. 9.2e-80;
Matches 275; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTCACAGCCCTGGGGGGCTCCGAGACCTCTCTGACG 71
QY 84 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 143
DB 72 CTCGTGATTCACCTTCATAGCTATAGCATGCTGCTCCGCGCAGGGTCCAGGAAGG 131
QY 144 GCTGAGTGGGTCTCATCTCATTTAGTATAGTAACTTACATATACGACGACGAGT 203
DB 132 GCTGAGTGGGTCTCATCTCATTTAGTATAGTAACTTACATATACGACGAGT 191
QY 204 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 263
DB 192 GAAGGGCCGATTCACCATCTCCAGACAGCCCAAGAACCTGATCTGCAATGAA 251
QY 264 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAG 307
DB 252 CAGCTGAGAGCCGACAGCAGCGCTGTGTACTACTGTGCGAGAG 295

RESULT 6

US-10-091-300-27
Sequence 27, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia

APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
FILE REFERENCE: 11245/46711
CURRENT APPLICATION NUMBER: US/10/091.300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 27
LENGTH: 348
TYPE: DNA
ORGANISM: Human
US-10-091-300-27

Query Match 68.6%; Score 269.6; DB 14; Length 348;
Best Local Similarity 96.8%; Pred. No. 9.2e-80;
Matches 275; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 71
QY 84 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 143
DB 72 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 131
QY 144 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 203
DB 132 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 191
QY 204 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 263
DB 192 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 251
QY 264 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAG 307
DB 252 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAG 295

RESULT 7

US-10-091-300-30
Sequence 30, Application US/10091300
Publication No. US20030108345A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091.300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 30
LENGTH: 348
TYPE: DNA
ORGANISM: Human
US-10-091-300-30

Query Match 68.2%; Score 268; DB 14; Length 348;
Best Local Similarity 96.5%; Pred. No. 3.2e-79;
Matches 274; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 71
QY 84 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 143
DB 72 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 131
QY 144 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 203
DB 132 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 191

DB 132 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 191
QY 204 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 263
DB 192 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 251
QY 264 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAG 307
DB 252 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAG 295

RESULT 8

US-10-325-694-143
Sequence 143, Application US/10325694
Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUFE, PETER
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
FILE REFERENCE: 3816400
CURRENT APPLICATION NUMBER: US/10/325.694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403.107
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 143
LENGTH: 414
TYPE: DNA
ORGANISM: HUMAN
US-10-325-694-143

Query Match 66.9%; Score 262.8; DB 12; Length 414;
Best Local Similarity 81.9%; Pred. No. 1.8e-77;
Matches 303; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTGACAG 71
QY 84 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 143
DB 72 CTCTGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 131
QY 144 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 203
DB 132 GCTGAGTCTGGTCTCATCTTATAGTATATATATATATATATATATATATATATATAT 191
QY 204 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 263
DB 192 GAAGGGCCGATTCACCTTCAGTAGCTATAGCATGACACTGGGTCGCCAGGAGTCCAGGAAGG 251
QY 264 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAGTCCAGGAAGG 323
DB 252 CAGCTGAGAGCCGAGACAGGCGCTGTGATCTATCTGTGAGAGTCCAGGAAGG 311
QY 324 TTTCCTGCTGGTGGTGGAGCCGAGTATGAGAGCTGTGGGGCCAGGAGCAGGTCAT 383
DB 312 TTTCCTGCTGGTGGTGGAGCCGAGTATGAGAGCTGTGGGGCCAGGAGCAGGTCAT 371
QY 384 CAGCTGCTCA 393
DB 372 CAGCTGCTCA 381

RESULT 9

US-10-041-860-59
Sequence 59, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadl
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-59

Query Match 66.5%; Score 261.2; DB 12; Length 379;
Best Local Similarity 83.5%; Pred. No. 6.1e-77;
Matches 309; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTCAGC 71
QY 84 CTGCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 143
DB 72 GCTGAGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 131
QY 144 GCTGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 203
DB 132 GCTGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 191
QY 204 GAAGGGCCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 263
DB 192 GAAGGGCCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 251
QY 264 CAGCTGAGAGCCGAGCAGCAGGCTGCTAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 323
DB 252 CAGCTGAGAGCCGAGCAGCAGGCTGCTAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 311
QY 324 TTTCCTCCGTTGGGTTCCGAGCAGCAGTATGAGCTGTGGGGCCCAAGGACCGGTCAT 383
DB 312 T---GCTGTTACTACTAGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGG 368
QY 384 CGTCTCTCA 393
DB 369 CGTCTCTCA 378

RESULT 10
US-10-041-860-75
Sequence 75, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadl
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 75

LENGTH: 382
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-75

Query Match 66.5%; Score 261.2; DB 12; Length 382;
Best Local Similarity 81.6%; Pred. No. 6.1e-77;
Matches 302; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCTGTCAGC 71
QY 84 CTGCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 143
DB 72 GCTGAGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 131
QY 144 GCTGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 203
DB 132 GCTGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 191
QY 204 GAAGGGCCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 263
DB 192 GAAGGGCCGATTCACTTCACTAGCTATAGCATGACATGCGGCTCCGCGAGGGTCCAGGAGG 251
QY 264 CAGCTGAGAGCCGAGCAGCAGGCTGCTAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 323
DB 252 CAGCTGAGAGCCGAGCAGCAGGCTGCTAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 311
QY 324 TTTCCTCCGTTGGGTTCCGAGCAGCAGTATGAGCTGTGGGGCCCAAGGACCGGTCAT 383
DB 312 TAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAA 371
QY 384 CGTCTCTCA 393
DB 372 CGTCTCTCA 381

RESULT 11
US-10-153-382-16
Sequence 16, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PEIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT FILING DATE: 2002-05-22
CURRENT APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 1413
TYPE: DNA
ORGANISM: Homo sapiens
US-10-153-382-16

Query Match 66.0%; Score 259.2; DB 14; Length 1413;
Best Local Similarity 81.0%; Pred. No. 4.6e-76;
Matches 316; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

QY 4 GTCGAGTCTGCTGAGTCTGGGGTGGAGTCTGGGGAGGCGTGGTCAAGCCTGGGGGGTCC 63
DB 49 GTCCAGTCTGAGTCTGAGTCTGGGGTGGAGTCTGGGGAGGCGTGGTCAAGCCTGGGGGGTCC 108
QY 64 CTGAGACTCTCTGTCAGGCTCTGGATTCACTTCACTAGCTATAGCATGACATGAGGTC 123
DB 109 CTGAGACTCTCTGTCAGGCTCTGGATTCACTTCACTAGCTATAGCATGACATGAGGTC 168
QY 124 CGCCAGGCTCCAGGAGGAGGCTGGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAA 183
DB 169 CGCCAGGCTCCAGGAGGAGGCTGGAGTGGGTCTCATCTATAGTAAATAGTAAATAGTAA 228

QY	18	ATTATTCAGCAGACGACCATGTAAGGCCGATTCACATCTCCAGAGCAACCCGCAAC	243
Db	229	AATATCTATGACAGACTCCGTGAAGGCCGATTCCACATCTCCAGAGCAATTCGAAC	288
QY	244	TCACCTATCTCAATGAACAGCCTGAGAGCCGACACAGCGCTGTCTACTACTGTGG	303
Db	289	ACCCTGATATGTGAATGTACAGCCTGTGAAGCCGAGACACAGCGCTGTGTATTACTGTGG	348
QY	304	AGAGATTCTAGATACAGTATATTCTCCGTGGGTGGGAGCGACGGTATGACGCTGG	363
Db	349	AGGAGATCCGAGGGGAGCTA-----CCCTTACTACTACTACTAGGATATGGAGCTGG	402
QY	364	GGCCAAGGAGACACGGTCTATGCTCTCTCA	393
Db	403	GGCCAAGGAGACACGGTCTACCGCTCTCTCA	432

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US-10-041-860-67
RESULT 12
US-10-041-860-67
Sequence 67: Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvahan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadl
APPLICANT: Weber, Richard
APPLICANT: Bezaheh, Biyham
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
TITLE OR INVENTION: THEREOF
FILE REFERENCE: AGENZIA_051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-67
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Query Match	65.68; Score 258; DB 12; Length 379;
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Best Local Similarity 83.0%; Pred. No. 7.1e-76;
Matches 307; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY	2	GGGAGAGTGTGGGGGGGCGCTGGTCAACCTGGGGGGGGCCCTGAGACTCTCTGTGGAGC	83
Db	12	GGTGGAGTGTGGGGGGGGCGGTGCTCACACTGTGGAGGTCCCTGAGACTCTCTGTGGAGC	71
QY	84	CTGTGATTCACCTTCAGTAGTATAGATGATCAGTGGGTCCGGCAGGGTCCAGGAAAGG	143
Db	72	GTCGTGATTCAGTTTCAGTAGCTATAGCGATGCACTGGSTCCGCCAGGCTCCAGGCAAGG	131
QY	144	GCCTGAGTGGGCTCATCTCATTAGTAATAGTAATTAATCTTACTATTAACGACAGCGACT	203
Db	132	GCTGGAGTGGGGTGGCGATATATGTGTATGATGGAAGTATATAATTAATCATATGACAGCTCCGT	191
QY	204	GAAGGGCCGATTCACCATCTCCAGACACAGCCACGAATCTACTGTATCTGCAAATGAA	263
Db	192	GAAGGGCCGATTCACCATCTCCAGACAAATTTCCAAAGAACGCTGTATCTGCAAATGAA	251
QY	264	CAGCCTGAGAGCCGAGCACAGCGCTGTACTACTGTCCGAGAGATTTCTGATACAGTAA	323
Db	252	CAGCCTGAGAGCCGAGGACACAGCGCTGTATTTATTTGTCCGAGAGATCAGGGATTAACGCTA	311
QY	324	TTTCTCCCTTGGGTTCCGAGGACGATGTAGAGTCTGGGGCCAAAGGACCAACGCTCAT	383
Db	312	TGTATTACGCTCT--ACTACGACTACGGTATGTGAGCTCTGGGGCCAAAGGACCAACGCTCAC	368
QY	384	CGTCTCTCTCA	393

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      Db              369 CGCTCCTCA 378          |||||
                                                    |
RESULT 13       US-09-844-684-10
? Sequence 10, Application US/09844684
? Patent No. US20020142358A1
? GENERAL INFORMATION:
? APPLICANT: GEMINI SCIENCE, INC.
? APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY OF MAKING SAME
? TITLE OF INVENTION: HUMAN ANTI -CD40 ANTIBODIES AND METHODS
? FILE REFERENCE: 21866/0276339
? CURRENT APPLICATION NUMBER: US/09/844,684
? PRIOR FILING DATE: 2001-04-27
? PRIOR APPLICATION NUMBER: US 60/200,601
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 10
? LENGTH: 520
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-844-684-10

```

Query Match 63.7%; Score 250.4; DB 10; Length 520;

Best Local Similarity 81.9%; Pred. NO. 2.7e-3;
Matches 303; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

24 GGTGAGTCTGGGGAGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG

[illegible][illegible]

84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACCTGGGTCGGCCAGGCTCCAGGGAAGG

Db 160 CTCTGGATTACCTTCAGTACCTACTGGATGCACCTGGGTCGCCAAGCTCCAGGGAAGG

14 GCTGGAGTGGTCTCATCCATTAGTAATAGTAATCTACATATACTACGACGACGAG

Db 220 GCTGGTGGGCTCACGTATTAAATAGTGAATGGAGTAGCACCAACCTACGGGACTCCGG

204 GAAGGCCGATTCACCACTCTCCAGAGACCAACGCCAAGAACTCACTGTATCTGCAATGA

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

DB 280 GAAGGCCGATTCACCATCTCCAGAGACCAAGCCAAAGAACACCGCTGTATCTGCATAATG

264 CAGCCTGAGAGCCGAGCACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTA

Db 340 CAGTCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCAAGAGATAGAGTACTATGGA

324 TTTCCTCCGTTGGGTTCCGAGCGACGGTATGGACGCTCTGGGGCCAAAGGACCACGGTCA

Db 399 -----TCGGGGAGTTATCCTACTACTACGGTATGGACGCTGGGGCCAAAGGACCACGGTCA

204 203

364 CGICCCCA 393
| | | | | | | | |
| | | | | | | | |

Db 454 CGTCTCCTCA 463

РЕСПУБЛИКА

RESOL 14
US-10-040-244-10

Sequence 10, Application US/10040244
Publication No. US20030059427A1

```

; GENERAL INFORMATION:
; ADDITIONAL: RTDN DEED KARDUCUUT VATECUA

```

APPLICANT: AARIN BEER KADOSHIN, AALSHA
; APPLICANT: FORCE, WALKER F.
;

APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI

; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTIMETABOLITES
; PRIORITY REFERENCE: 021386/0272501

FILE REFERENCE: 021200/0212001
CURRENT APPLICATION NUMBER: US/10/040,244

; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: 60/200,601

; PRIOR FILING DATE: 2000-4-28

;; PRIOR APPLICATION NUMBER: PCT/US01/13672
;; PRIOR FILING DATE: 2001-04-27
;; PRIOR APPLICATION NUMBER: 09/844,684
;; PRIOR FILING DATE: 2001-04-27
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 3.0
;; SEQ ID NO 10
;; LENGTH: 520
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-040-244-10

Query Match 63.7%; Score 250.4; DB 14; Length 520;
Best Local Similarity 81.9%; Pred. No. 2.7e-73;
Matches 303; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCTGGGGGCTCCCTGAGACTCTCTGTGCAGC 83
DB 100 GGTGAGTCTGGGGAGGCGCTGGTCAAGCTGGGGGCTCCCTGAGACTCTCTGTGCAGT 159
QY 84 CTCGTGATTCACTTCACTAGTATGATGACATGGGTCGGCCAGGGTCCAGGGAAGG 143
DB 160 CTCGTGATTCACTTCACTAGTATGATGACATGGGTCGGCCAGGTCCTCCAGGGAAGG 219
QY 144 GCTGAGTGGGTCTCATCTATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203
DB 220 GCTGAGTGGGTCTCATCTATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 279
QY 204 GAAGGCGCGATTCACTATCTCCAGACAGACAGCCCAAGACTCTCTGTGCAATGAA 263
DB 280 GAAGGCGCGATTCACTATCTCCAGACAGACAGCCCAAGACTCTCTGTGCAATGAA 339
QY 264 CAGCTGAGAGCGGACAGAGCGGTGTACTAGTCCGAGTTCTAGTACAGTAA 323
DB 340 CAGCTGAGAGCGGACAGAGCGGTGTACTAGTCCGAGTTCTAGTACAGTAA 398
QY 324 TTTCCTCCGTGGTTCGAGAGCGGTATGAGCTGTGGGGCCAAAGGAGACAGCGTCAT 383
DB 399 -----TCGGGGAGTTATCTACTACGTATGAGAGCTGTGGGGCCAAAGGAGACAGCGTCAC 453
QY 384 CGTCTCTCA 393
DB 454 CGTCTCTCA 463

RESULT 15

US-10-172-317-1
;; Sequence 1, Application US/10172317
;; Publication No. US20030091561A1
;; GENERAL INFORMATION:
;; APPLICANT: van de Wink, Jan G. J.
;; APPLICANT: van Dijk, Marcus A.
;; APPLICANT: Halk, Edward
;; APPLICANT: Gerltsen, Arnout F.
;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
;; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
;; FILE REFERENCE: GMI-020
;; CURRENT FILING DATE: 2002-06-13
;; PRIOR APPLICATION NUMBER: US/10/172,317
;; PRIOR FILING DATE: 2001-06-13
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 375
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-172-317-1

Query Match 63.3%; Score 248.8; DB 14; Length 375;
Best Local Similarity 81.6%; Pred. No. 8.3e-73;
Matches 302; Conservative 0; Mismatches 62; Indels 6; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGGTCAAGCTGGGGGCTCCCTGAGACTCTCTGTGCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGGTCAAGCTGGGGGCTCCCTGAGACTCTCTGTGCAGC 71
QY 84 CTCGTGATTCACTTCACTAGTATGATGACATGGGTCGGCCAGGGTCCAGGGAAGG 143
DB 72 GCTGAGTTCACCTTCACTAGTATGATGACATGGGTCGGCCAGGGTCCAGGGAAGG 131
QY 144 GCTGAGTGGGTCTCATCTATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203
DB 132 GCTGAGTGGGTCTCATCTATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 191
QY 204 GAAGGCGCGATTCACTATCTCCAGACAGACAGCCCAAGACTCTATGTAATGAA 263
DB 192 GAAGGCGCGATTCACTATCTCCAGACAGACAGCCCAAGACTCTATGTAATGAA 251
QY 264 CAGCTGAGAGCGGACAGAGCGGTGTACTAGTCCGAGAGATTTGTAGTACAGTAA 323
DB 252 CAGCTGAGAGCGGACAGAGCGGTGTACTAGTCCGAGAGATTTGTAGTACAGTAA 305
QY 324 TTTCCTCCGTGGTTCGAGAGCGGTATGAGCTGTGGGGCCAAAGGAGACAGCGTCAT 383
DB 306 TATGAGTGGGAGTTATGAGAGACTATTTGACTAGTGGGCGAGGAGACAGCGTCAT 365
QY 384 CGTCTCTCA 393
DB 366 CGTCTCTCA 375

RESULT 16

US-09-918-995-16657
;; Sequence 16657, Application US/09918995
;; Publication No. US20030073623A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc.
;; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;; FILE REFERENCE: 20411-756
;; CURRENT APPLICATION NUMBER: US/09/918,995
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: US/09/235,076
;; PRIOR FILING DATE: 1999-01-20
;; NUMBER OF SEQ ID NOS: 38054
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 16657
;; LENGTH: 407
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)-(407)
;; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-16657

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Best Local Similarity 94.5%; Pred. No. 1.6e-72;
Matches 257; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2000-09-27
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; LENGTH: 527
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; ORGANISM: Homo sapiens
US-09-954-456-1188
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; Sequence 73, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
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; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
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US-09-972-656-73
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Best Local Similarity 92.5%; Pred. No. 6.5e-72;
Matches 259; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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3	363.6	92.5	381	US-09-848-798-96	Sequence 96, Appl
4	363.6	92.5	381	US-09-848-798A-96	Sequence 96, Appl

5	272.2	69.3	311	36	US-09-864-761-3133	Sequence 3123, App
6	272.2	69.3	311	48	US-10-203-315-20914	Sequence 20914, App
7	272.2	69.3	311	48	US-10-203-316-21308	Sequence 21308, App
8	272.2	69.3	2091	47	US-10-170-73-3530772	Sequence 30772, App
9	272.2	69.3	200000	96	US-60-415-001-32	Sequence 32, App
10	272.2	69.3	375	68	US-60-415-001-3	Sequence 3, App
11	271.2	69.0	819	1	PCT-US02-18947-198	Sequence 198, App
12	271.2	69.0	819	1	PCT-US03-02612-6	Sequence 6, App
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15	271.2	69.0	819	45	US-10-172-118-198	Sequence 198, App
16	272.2	69.0	819	50	US-10-472-887-184	Sequence 887, App
17	270.8	68.9	379	102	US-60-474-850-84	Sequence 84, App
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ALIGNMENTS

RESULT 1
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Sequence 97, Application US/09848798
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09536-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

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? PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
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? SOFTWARE: PatentIn Ver. 2.0
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? OTHER INFORMATION: anti-Rh(D) chain E03
? IS-09-848-798-97

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QY	181	TTCATTAATCTAGGAGACGAGAGGAGGCGGATTCACATCTGCAGAGCAAGCAAGCCCAAG	240
Db	181	TTCATTAATCTAGGAGACGAGAGGAGGCGGATTCACATCTGCAGAGCAAGCAAGCCCAAG	240
QY	241	AACCTACGTGTATCTGCAAATGAACAGCCTGAGAGCCGAGCACAGCGCTGTGTATCTACTGT	300
Db	241	AACCTACGTGTATCTGCAAATGAACAGCCTGAGAGCCGAGCACAGCGCTGTGTATCTACTGT	300
QY	301	GGGAGAGATTCTAGATTACAGTAAATTTCTCTCGTTGGGTTGGAGAGCAAGGATATGAGAGTC	360
Db	301	GGGAGAGATTCTAGATTACAGTAAATTTCTCTCGTTGGGTTGGAGAGCAAGGATATGAGAGTC	360
QY	361	TGGGGCCAAAGGACCAAGCGTCACTGCTCTCA	393
Db	361	TGGGGCCAAAGGACCAAGCGTCACTGCTCTCA	393

RESULT 2

```

RESULT 2
US-09-848-798A-97
; Sequence 97, Application US/09848798A
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798A
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: 1999-05-02
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E03
; US-09-848-798A-97

```

Query Match	100.0%;	Score 393;	DB 35;	Length 393;
Best Local Similarity	100.0%;	Pred. No. 4.3e-105;		
Matches 393;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	GAGGTGCAGCTGCTGAGCTCTGGGGTGGAGTCTGGGGGGAGGCTGGTCAAGCTGGGGGG	60
Db	1	GAGGTGCAGCTGCTGAGCTCTGGGGTGGAGTCTGGGGGGAGGCTGGTCAAGCTGGGGGG	60
QY	61	TCCCTGAGACTCTCCTGTGCAGCCCTCTGGATTCACTTCATGAGCTATGATGCACCTGG	120
Db	61	TCCCTGAGACTCTCCTGTGCAGCCCTCTGGATTCACTTCATGAGCTATGATGCACCTGG	120
QY	121	GTCCGCCACGGTCCAGGGAGAAGGGGCTGGAGTGGGTCTCATTCATTATGTAATGTAATCT	180
Db	121	GTCCGCCACGGTCCAGGGAGAAGGGGCTGGAGTGGGTCTCATTCATTAGTAATGTAATCT	180
QY	181	TACATATCTACGCGAGCGAGCTGAAGGGCGGATTCACCATCTCCAGAGACAAAGCCAG	240
Db	181	TACATATCTACGCGAGCGAGCTGAAGGGCGGATTCACCATCTCCAGAGACAAAGCCAG	240
QY	241	AACCTCACTGTATCTGCAGTAATGAAACGCCCTGAGAGGCGAGACACAGGCTGTGACTACTGT	300
Db	241	AACCTCACTGTATCTGCAGTAATGAAACGCCCTGAGAGGCGAGACACAGGCTGTGACTACTGT	300
QY	301	GGGAGAGATTCTAGATACAGTATATTCTCCGTTGGGTTGGAGCGACGGTATGACGCTC	360
Db	301	GGGAGAGATTCTAGATACAGTATATTCTCCGTTGGGTTGGAGCGACGGTATGACGCTC	360
QY	361	TGGGGCCAAAGGACCAAGCGTATCCTCTCTCTCA	393
Db	361	TGGGGCCAAAGGACCAAGCGTATCCTCTCTCTCA	393

```

RESULT 3
US-09-848-798-96
: Sequence 96: Application US/09848798
: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/09/848,798
: PRIOR APPLICATION DATE: 2001-05-04
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 96
: LENGTH: 381
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain E01
US-09-848-798-96

```

Query Match	92.5%	Score 363.6	DB 35	Length 381
Best Local Similarity	98.9%	Pred. No. 2e-96		
Matches 366	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

Accession	Sequence	Position
QY	CTCTGGATTACACCTTCAGTAGCATATGCACCTGGGTCGCGCAGAGGTCACAGGAAAGG	143
Db	CTCTGGATTACACCTTCAGTAGCATATGCACCTGGGTCGCGCAGAGGTCACAGGAAAGG	131
QY	GGTGGAGTCTGGGGGAGGACCTGGTCAAGGCTGGGGGGTCCGAGACTCTCCGTGTACAC	83
Db	GCTCGAGTCTGGGGGAGGACCTGGTCAAGGCTGGGGGGTCCCTGAGACTCTCTGTGTACAC	71
QY	GCTGGAGTGGGCTCTCATTCATTAGTAATAGTAATCTTACATATATACACGAGCCAGT	203
Db	GCTGGAGTGGGCTCTCATTCATTAGTAATAGTAATCTTACATATATACGAGAGCCAGT	191
QY	GAAAGGCCGATTCACCATCTCCAGAGACAAAGCCCAAGAACTCACTATCTGCAATATGAA	263
Db	GAAAGGCCGATTCACCATCTCCAGAGACAAAGCCCAAGAACTCACTATCTGCAATATGAA	251

QY	261	CACCCGAGAGGCGACACACAGCGGCTGACTACGTCGAGAGATTCTGATACAGTAA	323
Db	252	CACCCGAGAGGCGAGGACACGCGTGCTACTACTGTGCGAGAAATTTCTGATACAATAA	311
OY	324	TTTTCCTCCGTTGGGTTCCGAGCGAGCGATGAGACGTGCGGGCCCAAGGGACAAGGTCAT	383
Db	312	TTTTCTCCGTTGGGTTCCGAGCGAGCGATGAGACGTCTGGGGCCCAAGGGACAAGGTCAT	371
OY	384	CGTCTCCTCA	393
Db	372	CGTCTCCTCA	381

```

RESULT 4
US-09-848-798A-96
: Sequence 96: Application US/09848798A
: GENERAL INFORMATION:
:   APPLICANT: Siegel, Donald L.
:   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
:   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
:   FILE REFERENCE: 09596-4202
:   CURRENT APPLICATION NUMBER: US/09/848,798A
:   CURRENT FILING DATE: 2001-05-04
:   PRIOR APPLICATION NUMBER: 09/240,274
:   PRIOR FILING DATE: 1999-05-02
:   PRIOR APPLICATION NUMBER: 60/028,550
:   PRIOR FILING DATE: 1996-10-11
:   NUMBER OF SEQ ID NOS: 224
:   SOFTWARE: PatentIn Ver. 2.0
:   SEQ ID NO 96
:   LENGTH: 381
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   OTHER INFORMATION: anti-Rh(D) chain E01
US-09-848-798A-96

```

Query Match	92.5%;	Score 363.6;	DB 35;	Length 381;
Best Local Similarity	98.9%;	Pred. No. 2e-96;		
Matches 366;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

QY	2	GGGAGAGCTCGGGGGAGGCGTGGTCAAGCCGAGGGGGGTCCTGAGACGCTCTGTGGAGC	83
Db	12	GCTCGAGCTCGGGGGAGGCGCTGGTCAAGCCTGAGGGGGTCCTGAGACTCTCTGTGGAGC	71
QY	84	CTCTGGAATTCACCTTCTAGTAGTATAGCATGCACATGGGTCCGCCAGGGTCCAGGGGAAGG	143
Db	72	CTCTGGAATTCACCTTCTAGTAGTATAGCATGTGACATGGGTCCGCCAGGGTCCAGGGGAAGG	121
QY	144	GCTGGAATGGGTCTCATCTTATGTAATGTAATCTTACTATATCTACGACAGCGAGT	203
Db	132	GCTGGAATGGGTCTCATCTTATGTAATGTAATCTTACTATATCTACGAGAGCGAGT	191
QY	204	GAAGGGCGGATTCACCATCTCCAGAGACAAAGCCAAAGCAACTGATCTGCAGAAATGA	263
Db	192	GAAGGGCGGATTCACCATCTCCAGAGACAAAGCCAAAGCAACTGATCTGCAGAAATGA	251
QY	264	CAGCCTGAGAGCCGAGACACAGGCGTGTACTACTGTCGAGAGATTCATGATACAGTAA	323
Db	252	CAGCCTGAGAGCCGAGAGACAGGCGTGTACTACTGTCGAGAGATTCATGATACAGTAA	311
QY	324	TTTCTCTCCGTTGGGTTCCGAGCGACGGTATGGAGCTCTGGGGCCAAAGGACACAGGTCA	383
Db	312	TTTCTCTCCGTTGGGTTCCGAGCGACGGTATGGAGCTCTGGGGCCAAAGGACACAGGTCA	371
QY	384	CGTCTCCTCA	393
Db	372	CGTCTCCTCA	381

RESULT 5
US-09-864-761-31233
; Sequence 31233, Application US/09864761

Db 143 GGTGAGTGGGTCTCATTCATTAGTAGTAGTAGTATACATATACAGCACTCACT 202
QY 204 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 263
Db 203 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 262
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 308
Db 263 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 307

RESULT 7
US-10-203-136-21308

; Sequence 21308, Application US/10203136
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 NO 3
; CURRENT APPLICATION NUMBER: US/10/203,136
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 21308
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019439.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW403220.1, EVALUE 0.00e+00
; FEATURE:
; OTHER INFORMATION: NT HIT: L29155.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUE 3.00e-43
; US-10-203-136-21308

Query Match

Best Local Similarity 69.3%; Score 272.2; DB 48; Length 311;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGTGGGAGGCGCTGTGCAAGCCTGGGGGTCCTGAGACTCTCTGTGCAGC 83
Db 23 GGTGAGTCTGTGGGAGGCGCTGTGCAAGCCTGGGGGTCCTGAGACTCTCTGTGCAGC 82
QY 84 CTCTGAGTTACCTTCACTAGCTATAGCATGATGCTGGTCCGCCAGGGTCCAGGGAAGGG 143
Db 83 CTCTGAGTTACCTTCACTAGCTATAGCATGATGCTGGTCCGCCAGGGTCCAGGGAAGGG 142
QY 144 GGTGAGTGGGTCTCATTCATTAGTAGTAGTAGTATACATATACAGCACTCACT 203
Db 143 GGTGAGTGGGTCTCATTCATTAGTAGTAGTAGTATACATATACAGCACTCACT 202

QY 204 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 263
Db 203 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 262
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 308
Db 263 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 307

RESULT 8
US-10-170-235-30772

; Sequence 30772, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
; FILE REFERENCE: CL001360
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 30772
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-170-235-30772

Query Match 69.3%; Score 272.2; DB 47; Length 2091;
Best Local Similarity 97.2%; Pred. No. 3.6e-69;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGTGGGAGGCGCTGTGCAAGCCTGGGGGTCCTGAGACTCTCTGTGCAGC 83
Db 128 GGTGAGTCTGTGGGAGGCGCTGTGCAAGCCTGGGGGTCCTGAGACTCTCTGTGCAGC 187
QY 84 CTCTGAGTTACCTTCACTAGCTATAGCATGATGCTGGTCCGCCAGGGTCCAGGGAAGGG 143
Db 188 CTCTGAGTTACCTTCACTAGCTATAGCATGATGCTGGTCCGCCAGGGTCCAGGGAAGGG 247
QY 144 GGTGAGTGGGTCTCATTCATTAGTAGTAGTAGTATACATATACAGCACTCACT 203
Db 248 GGTGAGTGGGTCTCATTCATTAGTAGTAGTAGTATACATATACAGCACTCACT 307
QY 204 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 263
Db 308 GAAGGGCCGATTACCATCTCCAGAGACAAAGCAAGCACTGATCTGCATATGAA 367
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 308
Db 368 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGA 412

RESULT 9
US-60-415-024-32

; Sequence 32, Application US/60415024
; GENERAL INFORMATION:
; APPLICANT: Jolly, Chris
; TITLE OF INVENTION: Immunoglobulin Compositions and Methods
; FILE REFERENCE: 13311.1001
; CURRENT APPLICATION NUMBER: US/60/415,024
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 200000
; TYPE: DNA
; ORGANISM: Human
; US-60-415-024-32

Query Match

Best Local Similarity 69.3%; Score 272.2; DB 96; Length 200000;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 24 GGTGAGTCTGTGGGAGGCGCTGTGCAAGCCTGGGGGTCCTGAGACTCTCTGTGCAGC 83

Db	197586	GGTGGAGTGTGGGGGAGGCGCTGGTCAACCTGGGGGGGCTCTGGAGACTCTCTTCGAGC	197645
Qy	84	CTCTGATTCACGCTTCAGTAGCTATAGCATGCACACGGGTCTCGCAGGATCCAGGAAGGG	143
Db	197646	CTCTGGATTACACTTCAGTAGCTATAGCATGTAACTGAGGGTCCGCCAGGCTCCAGGAAGGG	197705
Qy	144	GGCGAGTGGGGTCTCATCATAGTAATAGTAATATCTTACATATACGACAGCGAGT	203
Db	197706	GCTGAGTGGGTCTCATCTCATTAGTAGTAGTAGTATCTTACATATACGACAGCGAGT	197765
Qy	204	GAAGGGCGATTCACCATCTCCAGAGACAAGCCCAAGACTCACTGTATCTGCAATGAA	263
Db	197766	GAAGGGCCCATTCACCATCTCCAGAGACAAGCCCAAGACTCACTGTATCTGCAATGAA	197825
Qy	264	CAGCCGTAGAGCGGAGACACGCGGTGTACTACTGTCGAGACA	308
Db	197826	CAGCCGTAGAGCGGAGACAAGCGGTGTATTTACTGTGCGAGACA	197870

RESULT 10
US-60-141-701-3
; Sequence 3, Application US/60141701
; GENERAL INFORMATION:

```

1 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HIV-1 ENVELOPE
2
3 TITLE OF INVENTION: GLYCOPROTEIN GP120
4
5 FILE REFERENCE: 2026-4284
6
7 CURRENT APPLICATION NUMBER: US/60/141,701
8
9 CURRENT FILING DATE: 1999-06-30
10
11 NUMBER OF SEQ ID NOS: 100
12
13 SOFTWARE: PatentIn Ver. 2.1
14
15 SEQ ID NO 3
16
17 LENGTH: 375
18
19 TYPE: DNA
20
21 ORGANISM: Human Immunodeficiency virus type 1
22
23 FEATURE:
24
25 OTHER INFORMATION: VH
26
27 US-60-141-701-3

```

Query Match	69.2%	DB 68	Length 375;
Best Local Similarity	86.1%	Pred. No. 2.7e-69;	
Matches 316; Conservative	0;	Mismatches 42;	Indels 9; Gaps 1.

[illegible]

RESULT 11
PCT-US02-18947-198
Sequence 198, Application PC/TUS0218947
GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
FILE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 60/380,770
PRIORITY FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 198
LENGTH: 819
TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION:
DATABASE ACCESSION NUMBER: AJ225092
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-198

PCT-US02-18947-198

Query Match	69.0%;	Score 271.2;	DB 1;	Length 819;
Best Local Similarity	86.2%;	Pred. No. 5.2e-69;		
Matches 319;	Conservative 0;	Mismatches 33;	Indels 18;	Gaps 1.

QY	24	GGGAGAGTGTGGGGGAGGCGTGTCTAAACCCCTGGGGGGGTCCTGAGACATCTCTGTGAGC	83
Db	18	GGGAGAGTGTGGGGGAGGCGTGTCTAAACCCCTGGGGGGGTCCTGAGACATCTCTGTGAGC	77
QY	84	CTCTGATTTACCTTCAGTAGCTATATAGCATATCAGTGGGTCCGCGAGGGTCAGAGAAAGG	143
Db	78	CTCTGATTTACCTTCAGTAGCTATATAGCATATCAGTGGGTCCGCGAGGGTCAGAGAAAGG	137
QY	144	GGTGGAGTGGGTCTCATCCATTAGTAATAGTAATATCTTACTATACGACAGCGAGT	203
Db	138	GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATATCTTACTATACGACAGCTTGGT	197
QY	204	GAAGGGCGATTACCATCTCCAGAGACAAGCCCAAGAACATCATGTATGTGCAANTGA	283
Db	198	GAAGGGCGATTACCATCTCCAGAGACAAGCCCAAGAACATCATGTATGTGCAANTGA	257
QY	264	CAGCCGTAAAGCGAGACAGCGGTCTACTACTGTGGCGAGAAATTTCTAGATACAGTA	323
Db	258	CAGCCGTAAAGCGAGACAGCGGTCTACTACTGTGGCGAGAAATTTCTAGATACAGTA	300
QY	324	TTTTCCTCCGTTGGGTTCCGAGCGACGATATGAGACGTCTGGGGCCCAAGGACACACGTCAT	383
Db	301	-TCCAGTATTACGATTTTGTGTGGGGATGAGAGCTCTGGGGCAGAGGCAACCTGGTCA	359
QY	384	CGTCTCTCTCA	393
Db	360	CGTCTCTCTCA	369

RESULT 12

```

Sequence: 6, Application PC/TUS0302612
GENERAL INFORMATION:
APPLICANT: Egea Biosciences, Inc.
APPLICANT: Evans, Glen A.
TITLE OF INVENTION: Methods for Creating Recombination
TITLE OF INVENTION: Products Between Nucleotide Sequences
FILE REFERENCE: EP-EA 5505
CURRENT APPLICATION NUMBER: PCT/US03/02612
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 10/062,188
PRIOR FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 819
TYPE: DNA

```



```

: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: synthetic construct
:
: FEATURE:
:
: NAME/KEY: CDS
: LOCATION: (7)...(777)
:
: PCT-US03-02612-6

```

Query Match	69.0%;	Score 271.2;	DB 1;	Length 819;
Best Local Similarity	86.2%;	Pred. No. 5.2e-69;		
Matches 319; Conservative	0;	Mismatches 33;	Indels 18;	Gaps 1;

QY	24	GGTGGAGTGTGGGGGAGGCGCTGGTCAACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC	83
Db	18	GGTGGAGTGTGGGGGAGGCGCTGGTCAACCTGGGGGGTCCCTGAGACTCTCTGTGCAGC	77
QY	84	CTCTGGATTACACCTTCAGTAGCTATAGCATGCACCTGGGTCCGCGAGGGTCCAGGAAAGG	143
Db	78	CTCTGGATTACACCTTCAGTAGCTATAGCATGCACCTGGGTCCGCGAGGGTCCAGGAAAGG	137
QY	144	GCTGGAGTGGGTCTATCCATTAGTAATAGTAATACTTACTATATCTACGACGACGACT	203
Db	138	GCTGGAGTGGGTCTATCCATTAGTAATAGTAATAGTAATACTTACTATACGACGACGCTCGT	197
QY	204	GAAGGGCCGATTACACCATCTCCAGAGACAAAGCCAAAGCACTGTATGTGCAAATGAA	263
Db	198	GAAGGGCCGATTACACCATCTCCAGAGACAAAGCCAAAGCACTGTATGTGCAAATGAA	257
QY	264	CAGCCTGAGAGCCGAGACACAGCGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA	323
Db	258	CAGCCTGAGAGCCGAGAGACAGCGCTGTGTATTACTGTGCGAGA-----	300
QY	324	TTTCTCGCTGGGTTCCGAGCGACGGATGAGACTGTGGGGCCAAAGGACACAGTCAT	383
Db	301	-TCCATATTAGATTTTGTGTGGCGGTATGTGACGTGTGGGGCAGAGGACCTCGGTGCAC	359
QY	384	CGTCTCCACA	393
Db	360	CGTCTCTCA	369

```

RESULT 13
PCT-US03-02612-6
: Sequence 5, Application FC/TUS0302612
: GENERAL INFORMATION:
: APPLICANT: Egea Biosciences, Inc.
: APPLICANT: Evans, Glen A.
: TITLE OF INVENTION: Methods For Creating Recombination

```

```

1 CURRENT APPLICATION NUMBER: PCT/US03/02612-6
2
3 CURRENT FILING DATE: 2003-01-29
4
5 PRIOR APPLICATION NUMBER: US 10/062,188
6
7 PRIOR FILING DATE: 2002-01-30
8
9 NUMBER OF SEQ ID NOS: 231
10
11 SOFTWARE: FastSeq for Windows Version 4.0
12
13 SEQ ID NO 6
14
15 LENGTH: 819
16
17 TYPE: DNA
18
19 ORGANISM: Artificial Sequence
20
21 FEATURE:
22
23 OTHER INFORMATION: synthetic construct
24
25 FEATURE:
26
27 NAME/KEY: CDS
28
29 LOCATION: (77)...(777)
30
31 CDT-US03-02612-6

```

Query Match	69.0%	Score 271.2	DB 2	Length 819
Best Local Similarity	86.2%	Pred. No. 5.2e-69		
Matches 319	Conservative 0	Mismatches 33	Indels 18	Gaps 1
QY	24	GGTGGACTCTGGGGGAGGCCCTGGTCAACCCCTGGGGGCTCTGGAACACTCTCTGTGCACG	83	

[illegible]

```

RESULT 14
US-10-062-188-6
? Sequence 6: Application US/10062188
?
? GENERAL INFORMATION:
?
? APPLICANT: Evans, Glen A.
?
? TITLE OF INVENTION: Methods For Creating Recombination
?
? TITLE OF INVENTION: Products Between Nucleotide Sequences
?
? FILE REFERENCE: P-EA 5008
?
? CURRENT APPLICATION NUMBER: US/10/062,188
?
? CURRENT FILING DATE: 2001-01-31
?
? NUMBER OF SEQ ID NOS: 231
?
? SOFTWARE: FastSeq for Windows Version 4.0
?
? SEQ ID NO 6
?
? LENGTH: 819
?
? TYPE: DNA
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: synthetic construct
?
? NAME/KEY: CBS
?
? LOCATION: (77)...(777)
?
? US-10-062-188-6

```

Query Match	69.0%;	Score 271.2;	DB 45;	Length 819;
Best Local Similarity	86.2%;	Pred. No. 5.2e-69;		
Matches 319; Conservative	0;	Mismatches 33;	Indels 18;	Gaps 1

OY	84	CTCTGGATTACCCTTTCAAGTAGCTATAGCATGCACTGGGTGCCCGCAGGGTCCAGGGAAAGG	143
Db	18	GGTGGAGTGTGGGGGAGGAGGCTTGATGAAGCTTGGGGGGTCCTTGAGACTCTCTCTGGCACG	77
OY	78	CTCTGGATTACACCTTCAGTAACCTATAGCATGAACTGGGTCCGCAGGCTCCAGGGAAAGG	137
Db	144	GCTGGAGTGGGTCTATCCATTAGTAATAATATCTTACTACATATCTACGACGACGCGAT	203
OY	138	GCTGGAGTGGGTCTATCCATTAGTAATAATATCTTACTACATATCTACGACGACGCTCGT	197
Db	204	GAAAGGCGCATTCACCATCTCCAGAGACAAGCCAGAAGCACTCATGTATCTGCAAAATGAA	265
OY	198	GAAAGGCGCATTCACCATCTCCAGAGACAAGCCAGAAGCACTCATGTATCTGCAAAATGAA	257
Db	264	CAGCCTGAGAGCCGAGACACAGCGGCTGTACTACTGTGCGAGAGATTCCTAGATACAGTAA	323
OY	258	CAGCCTGAGAGCCGAGAGACAGCGGCTGTATCTACTGTGCGAG-----	300

SEQ ID NO 84
LENGTH: 819
TYPE: DNA
ORGANISM: Homo sapiens
US-60-474-850-84

Query Match 69.0%; Score 271.2; DB 102; Length 819;
Best Local Similarity 86.2%; Pred. No. 5.2e-69;
Matches 319; Conservative 0; Mismatches 33; Indels 18; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 83
DB 18 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 77
QY 84 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 143
DB 78 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 137
QY 144 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203
DB 138 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 197
QY 204 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 263
DB 198 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 257
QY 264 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 323
DB 258 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 300
QY 324 TTTCCTCCGTTGGGTTCCGAGCGAGTATGAGCTGTGGGGCCCAAGGACCGCTCAT 383
DB 301 -TTCAGTATATGATTTTGGTGGGGTATGAGCTGTGGGGCCCAAGGACCGCTCAT 359
QY 384 CGTCTCTCA 393
DB 360 CGTCTCTCA 369

RESULT 18

PCT-US03-00398-55
Sequence 55, Application PC/TUS0300398
GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: JIA, Xiao-Chi
APPLICANT: FENG, Xiao
APPLICANT: YANG, Xiao-Dong
APPLICANT: CHEN, Francine
APPLICANT: GAZIT, Gadl
APPLICANT: WEBER, Richard
APPLICANT: BEZABEH, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REFERENCE: ABGENIX.051VPC
CURRENT APPLICATION NUMBER: PCT/US03/00398
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
PCT-US03-00398-55

Query Match 68.9%; Score 270.8; DB 1; Length 379;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 315; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 71
QY 84 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 143

DB 72 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 131
QY 144 GGTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203
DB 132 GGTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 191
QY 204 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 263
DB 192 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 251
QY 264 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 323
DB 252 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 308
QY 324 TTTCCTCCGTTGGGTTCCGAGCGAGTATGAGCTGTGGGGCCCAAGGACCGCTCAT 383
DB 309 GTTGGGGGAATTAATAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 368
QY 384 CGTCTCTCA 393
DB 369 CGTCTCTCA 378

RESULT 19

PCT-US03-00398-55
Sequence 55, Application PC/TUS0300398
GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: JIA, Xiao-Chi
APPLICANT: FENG, Xiao
APPLICANT: YANG, Xiao-Dong
APPLICANT: CHEN, Francine
APPLICANT: GAZIT, Gadl
APPLICANT: WEBER, Richard
APPLICANT: BEZABEH, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REFERENCE: ABGENIX.051VPC
CURRENT APPLICATION NUMBER: PCT/US03/00398
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
PCT-US03-00398-55

Query Match 68.9%; Score 270.8; DB 2; Length 379;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 315; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTGTCAGCCCTGGGGGGCTCCCTGAGACTCTCTGTGCAGC 71
QY 84 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 143
DB 72 CTCGTGATTCACCTTCACTAGTCTATAGCATGACAGTGGGTCCGCGAGGCTCCAGGAAAGG 131
QY 144 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203
DB 132 GCTGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 191
QY 204 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 263
DB 192 GAAGGCGCGATTCACCATCTCCAGAGACAGCCAGAACCTCAGTCTGTGCAATGAA 251
QY 264 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 323
DB 252 CAGCTGAGAGCCGAGACAGCGCTGTGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAG 308

Wed Sep 24 09:31:33 2003

us-09-848-798a-97.rtf

Page 10

QY	32	TTTCCCTCCCTTGGGTTGCGAGACGGATGACGTCGGGGCCCAAGGACCAAGGTCAT	383
QY	32	TTTTTCCCTCCCTTGGGTTGCGAGACGGATGACGTCGGGGCCCAAGGACCAAGGTCAT	383
Db	309	GTTTGGGGGAATTATTCGCGCTCGTTCTACTTGGACTAGGCGCCAGGAAACCTCGTCTAC	368
QY	384	CGTCCTCTCA	393
Db	369	CGTCTCTCA	378

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RESULT 20
US-10-041-860-55
: Sequence 55, Application US/10041860
: GENERAL INFORMATION:
: APPLICANT: Corvelan, Jose R.F.
: APPLICANT: Jia, Xiao-Chi
: APPLICANT: Feng, Xiao
: APPLICANT: Yang, Xiao-Dong
: APPLICANT: Chen, Francine
: APPLICANT: Gazit, Gadi
: APPLICANT: Weber, Richard
: APPLICANT: Bezaleh, Binyam
: TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
: THEREOF
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: ABGEN1A.051A
: CURRENT APPLICATION NUMBER: US/10/041,860
: NUMBER OF SEQ ID NOS: 377
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 55
: LENGTH: 379
: TYPE: DNA
: ORGANISM: homo sapiens
: US-10-041-860-55

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Query Match	68.9%;	Score 270.8;	DB 44;	Length 379;
Best Local Similarity	85.1%;	Pred. No. 5.4e-69;		
Matches 315; Conservative	0;	Mismatches 52;	Indels 3;	Gaps 1;

QY	2	GGTGGAGTCTGGGGGAGGCGCTGTGTCAGACCGCTGGGGGGGTCCCTGAGACTCTCCGTGCAC	83
Db	12	GTTGGAGTCTGGGGGAGGCGCTGTGTCAGACCGCTGGGGGGTCCCTGAGACTCTCTGTGCAC	71
QY	84	CTCTGGATTCAACCTTCAGTACTAGCTTAGAGTGCACATGGTCTCCGACAGGCTCCAGGAAAGG	143
Db	72	CTCTGGATTCAACTTCAGACCTTAACTATGAACTGGGTCTCCGACAGGCTCCAGGAAAGG	131
QY	144	GCTGGAGTGGGGTTCATCTCATTAAATAGTAATAGTAATCTAACTAACTAGCAGAACGCACT	203
Db	132	GCTGGAGTGGGGTTCATCTCATTAAATAGTAACTAGTAACTAACTAACTAGCAGAACGCACT	191
QY	204	GAAAGGCCGATTCACATCTCCAGAGCAACGCCAAGAACTCACTGATTTGCAATGAA	263
Db	192	GAAAGGCCGATTCACATCTCCAGAGCAACGCCAAGAACTCACTGATTTGCAAAATGAA	251
QY	264	CAGCCTGAGAGCCCGAGCACACGCGTGTGTACTACTGTGCAGAGATTTAGATPACAGTAA	323
Db	252	CAGCCTGAGAGCCCGAGCACACGCGTGTGTATTTACTGTGCAGAGATTTA --- TGAATTAC	308
QY	324	TTTCTCTCCGTTGGGTTCCGAGCGACGGTATGAGACGTCGTGGGGCCAAAGGACACCGGTCA	383
Db	308	TTTCTCTCCGTTGGGTTCCGAGCGACGGTATGAGACGTCGTGGGGCCAAAGGACACCGGTCA	368
QY	384	CGTCTCTCTCA 393	
Db	368	CGTCTCTCTCA 378	

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Job time : 3361 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2003, 03:27:44 ; Search time 864 Seconds
(without alignments)
554.003 Million cell updates/sec

Title: US-09-848-798A-97
Perfect score: 393
Sequence: 1 gaggtgcagctgcctcagtc.....ccacgctcctcctca 393

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 960753 seqs, 608980626 residues
Total number of hits satisfying chosen parameters: 1921506

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

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3: /cgn2-6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2-6/ptodata/2/pna/US08_NEW_COMB.seq:*
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7: /cgn2-6/ptodata/2/pna/US50_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273.6	69.6	369	1	PCT-US03-21304-3 Sequence 3, Appl1
2	248	63.1	747	1	PCT-US03-25457-65 Sequence 65, Appl1
3	247.6	63.0	741	1	PCT-US03-23826-46 Sequence 46, Appl1
4	246.6	62.2	469219	7	US-60-495-114-16704 Sequence 16704, A
5	239.8	61.0	436	1	PCT-US03-26322-145 Sequence 145, App
6	236.8	60.3	510	6	US-10-469-304-16 Sequence 16, Appl1
7	233.4	59.4	360	1	PCT-US02-34154-19 Sequence 19, Appl1
8	233.4	59.4	360	6	US-10-456-092A-19 Sequence 19, Appl1
9	233.4	59.4	1430	1	PCT-US02-26584-1 Sequence 1, Appl1
10	233.8	59.2	357	6	PCT-US02-34154-20 Sequence 20, Appl1
11	232.8	59.2	357	6	US-10-456-092A-20 Sequence 20, Appl1
12	231.6	58.9	393	1	PCT-US03-15937-52 Sequence 52, Appl1
13	231.2	58.8	867	5	US-09-194-164-16 Sequence 16, Appl1
14	231.2	58.8	918	5	US-09-194-164-13 Sequence 13, Appl1
15	231.2	58.8	918	5	US-09-194-164-15 Sequence 15, Appl1
16	230	58.5	372	6	US-10-031-722A-1 Sequence 1, Appl1
17	229.6	58.4	867	5	US-09-194-164-18 Sequence 18, Appl1
18	227	57.8	360	5	US-09-848-350-121 Sequence 121, App
19	226	57.5	366	6	US-10-031-722A-5 Sequence 5, Appl1
20	225.8	57.5	352	1	PCT-US03-25161-17 Sequence 17, Appl1
21	225.6	57.4	417	6	US-10-656-769-9 Sequence 9, Appl1
22	225.6	57.4	1395	6	US-10-656-769-21 Sequence 21, Appl1
23	225.6	57.4	1398	6	US-10-656-769-23 Sequence 23, Appl1
24	225.6	57.4	1407	6	US-10-656-769-19 Sequence 19, Appl1
25	225.2	57.3	351	1	PCT-US03-21304-4 Sequence 4, Appl1
26	224.4	57.1	908	6	US-10-375-356A-9 Sequence 9, Appl1

27	224	57.0	366	6	US-10-031-722A-9 Sequence 9, Appl1
28	224	57.0	903	6	US-10-375-356A-12 Sequence 12, Appl1
29	224	57.0	913	6	US-10-375-356A-10 Sequence 10, Appl1
30	223.6	56.9	351	1	PCT-US03-21304-5 Sequence 5, Appl1
31	223.6	56.9	351	1	PCT-US03-21304-6 Sequence 6, Appl1
32	222	56.5	351	1	PCT-US03-21304-7 Sequence 7, Appl1
33	220.8	56.2	417	6	US-10-656-769-13 Sequence 13, Appl1
34	220.8	56.2	1395	6	US-10-656-769-27 Sequence 27, Appl1
35	220.8	56.2	1398	6	US-10-656-769-29 Sequence 29, Appl1
36	220.8	56.2	1407	6	US-10-656-769-25 Sequence 25, Appl1
37	220.4	56.1	351	1	PCT-US03-21304-8 Sequence 8, Appl1
38	220.4	56.1	351	1	PCT-US03-21304-9 Sequence 9, Appl1
39	219.4	55.8	1392	6	US-10-645-215-7 Sequence 7, Appl1
40	218.8	55.7	351	1	PCT-US03-21304-10 Sequence 10, Appl1
41	217.2	55.3	369	1	PCT-US03-19333-25 Sequence 25, Appl1
42	214.8	54.7	345	1	PCT-US03-21304-11 Sequence 11, Appl1
43	213.6	54.4	345	1	PCT-US03-21304-15 Sequence 15, Appl1
44	213	54.2	743	5	US-09-538-038A-2352 Sequence 2352, Ap
45	212.4	54.0	892	6	US-10-375-356A-11 Sequence 11, Appl1
46	212	53.9	345	1	PCT-US03-21304-13 Sequence 13, Appl1
47	211.6	53.8	411	1	US-09-538-038A-2350 Sequence 2350, Ap
48	211	53.7	752	5	PCT-US03-10749A-37 Sequence 37, Appl1
49	209.6	53.3	363	1	PCT-US03-22566-37 Sequence 37, Appl1
50	209.6	53.3	1493	1	PCT-US03-18934-94 Sequence 94, Appl1
51	208.8	53.1	345	1	PCT-US03-21304-12 Sequence 12, Appl1
52	208.2	53.0	348	1	PCT-US03-10749A-13 Sequence 13, Appl1
53	208.2	53.0	369	1	PCT-US02-30316-1 Sequence 1, Appl1
54	208.2	53.0	1413	1	PCT-US03-10749A-37 Sequence 37, Appl1
55	207.8	52.9	369	1	PCT-US03-19333-27 Sequence 27, Appl1
56	207.2	52.7	358	1	PCT-US03-25161-73 Sequence 73, Appl1
57	206.4	52.5	738	1	PCT-US03-19333-33 Sequence 33, Appl1
58	205.6	52.3	345	1	PCT-US03-21304-14 Sequence 14, Appl1
59	204.8	52.1	432	6	US-10-257-864A-66 Sequence 66, Appl1
60	204.8	52.1	738	1	PCT-US03-19333-30 Sequence 30, Appl1

ALIGNMENTS

RESULT 1
PCT-US03-21304-3
; Sequence 3, Application PC/TUS0321304
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053893-5050WO
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-21304-3

Query Match Best Local Similarity 69.6%; Score 273.6; DB 1; Length 369;
Matches 319; Conservative 0; Mismatches 39; Indels 12; Gaps 1;

QY	24	GGTGGAGTCTGGGGGAGGCTGGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGCAGC	83
DB	12	GGTGGAGTCTGGGGGAGGCTGGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGCAGC	71
QY	84	CTCTGGATTCACCTTCATAGCTATAGCATGTGACTGGGTCCGCCAGGGTCCAGGAAGG	143
DB	72	CTCTGGATTCACCTTCATAGCTATAGCATGTGACTGGGTCCGCCAGGGTCCAGGAAGG	131


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PCT-US02-34154-19
; Sequence 19, Application PC/TUS0234154
; GENERAL INFORMATION:
; APPLICANT: Centocor Inc.
; TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0203PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34154
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/336081
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-34154-19

Query Match
Best Local Similarity 59.4%; Score 233.4; DB 1; Length 360;
Matches 255; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 25 GTGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGCC 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 16 GAGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGCC 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 85 TCTGATTCACCTTCAGTACCTATAGCATGACGCTGGGTCGCCAGGATCCAGGAGGG 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 76 TCTGAGACCAACCCCTAGTGGCTATATACATGACGCTGGGTCGCCAGGATCCAGGAGGG 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 145 CTGAGAGGGTCTATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGAGT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 136 CTGAGTGGGTCTATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGAGT 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 205 AAGGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAC 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 AAGGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAC 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 265 AGCTGAGAGCCGAGCAGCGGTGTACTACTCTGTCCGAGAAATCTAGA 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 AGCTGAGAGCCGAGCAGCGGTGTACTACTCTGTCCGAGAAATCTAGA 306
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RESULT 8
US-10-456-092A-19
; Sequence 19, Application US/10456092A
; GENERAL INFORMATION:
; APPLICANT: Centocor Inc.
; TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0203USNP
; CURRENT APPLICATION NUMBER: US/10/456, 092A
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/336081
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-456-092A-19

Query Match
Best Local Similarity 87.6%; Pred. No. 9.4e-63;
Matches 255; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 25 GTGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGCC 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 16 GAGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGCC 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 85 TCTGATTCACCTTCAGTACCTATAGCATGACGCTGGGTCGCCAGGATCCAGGAGGG 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 76 TCTGAGACCAACCCCTAGTGGCTATATACATGACGCTGGGTCGCCAGGATCCAGGAGGG 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 145 CTGAGAGGGTCTATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGAGT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 136 CTGAGTGGGTCTATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGAGT 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 205 AAGGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAC 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 AAGGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAC 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 265 AGCTGAGAGCCGAGCAGCGGTGTACTACTCTGTCCGAGAAATCTAGA 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 AGCTGAGAGCCGAGCAGCGGTGTACTACTCTGTCCGAGAAATCTAGA 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
PCT-US02-26584-1
; Sequence 1, Application PC/TUS0226584
; GENERAL INFORMATION:
; APPLICANT: Hoeper, Craig
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; FILE REFERENCE: 8321-110 PC
; CURRENT APPLICATION NUMBER: PCT/US02/26584
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-26584-1

Query Match
Best Local Similarity 79.1%; Pred. No. 1.5e-62;
Matches 292; Conservative 0; Mismatches 71; Indels 6; Gaps 1;

OY 24 GGTGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGC 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 72 GTTGGAGTCTGGGGAGGCTGTGTCAGCCCTGGGGGGTCCCTGAGACTCTCTGTGAGC 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 84 CTCTGATTCACCTTCAGTACCTATAGCATGACGCTGGGTCGCCAGGATCCAGGAGGG 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 CTCTGATTCACCTTCAGTACCTATAGCATGACGCTGGGTCGCCAGGATCCAGGAGGG 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 144 GCTGAGTGGTCTCATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGCAGT 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 GCTGAGTGGTCTCATCATCTAGTAATAGTAATCTACTATACATGAGAGGAGCAGT 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 204 GAAGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAA 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 252 GAAGGCCGATTCACATCTCCAGAGACAGCCCAAGCACTGATCTGCAAAATGAA 311
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 264 CAGCTGAGAGCCGAGCAGCGGTGTACTACTGTGCGAGAGATCTGATATACAGTAA 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 312 CAGCTGAGAGCCGAGCAGCGGTGTACTACTGTGCGAGAGATCTGATATACAGTAA 371
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 324 TTTCTCTCGTTGGTGGAGCGAGCGGTATGAGAGCGTGTGGGCAAGGACAGGTCAT 383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 372 GATAGT-----TGTACTTAATGAGAGCTTGTACTACTGTGGGCGAGGAAACCCGGGTAC 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 384 CGTCTCTTC 392
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 426 CGTCTCTTC 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
PCT-US02-34154-20
; Sequence 20, Application PC/TUS0234154
```


Wed Sep 24 09:31:34 2003

us-09-848-798a-97.rnp

Page 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,164
FILING DATE: 09-Apr-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813500
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: join(1..855, 862..867)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

15-09-194-164-16

```

US-09-194-164-13
? Sequence 13, Application US/09194164
? GENERAL INFORMATION:
? APPLICANT: Dan, Michael D.
? Kaplan, Howard A.
? Malt, Pradip K.
? TITLE OF INVENTION: ANTIGENICALLY BINDING FRAGMENTS THAT
? SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING
? FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
? DETECTION OF CANCERS
?
? NUMBER OF SEQUENCES: 18
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Morrison & Foerster
? STREET: 755 Page Mill Road
? CITY: Palo Alto
? STATE: CA USA
? COUNTRY: USA
? ZIP: 94304-5018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/194,164
? FILING DATE: 09-Apr-1999
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/657,449
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Lehnhardt, Susan K.
? REGISTRATION NUMBER: 33,943
? REFERENCE/DOCKET NUMBER: 31608-20001.00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 813-5600
? TELEFAX: (415) 494-0792
? TELEX: 706141
?
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 918 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? FEATURE:
? NAME/KEY: CDS
? LOCATION: join(1..906, 913..918)
? SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-194-164-13
?
? Query Match 58.8%; Score 231.2; DB: 5; Length 918;
? Best Local Similarity 78.6%; Freq: No. 6.2e-62;
? Matches 291; Conservative 0; Mismatches 73; Indels 6; Gaps 1;
?
?
? 24 GGTGAGTCTGGGGGAGGCCCTGTCGACCGCGGGGGGTCCTCGAGAGCTCTCTGCGAGC 83
? 489 GGTGAGTCTGGGGGAGGGGCGTGCTCCACCTGGGAGGTCCCTGAGAGCTCTCTGCGAGC 548
?
? 84 CTCTGATTCACCTTACCTAGCTATAGATGACACTGGGCGCGCCAGGGGTCCAGGAAAGG 143
? 549 CTCTGATTCACCTTACCTTCCAGAGCTTTGCTATGCTACTGGGCGCGCCAGGGCTTACGCAAGG 608
?
? 144 GCTGAGTGGGTCTATCCATAGTAATATGTAATCTTACATATCTACTACAGCAGACGCACT 203
? 609 GCTGAGTGGGTGGGCGAGTTATATCATATGATGAGACATAAATACTACGACAGCTCCGT 668
?
? 204 GAAGGCGCCATCACCTATCGACGAGACACAAGCGACAGAGCTACATGTATCTCCAAATGAA 263
? 669 GAAGGCGCCATTCACCATCTCCAGAGACACTTCCAGAGACACGGGTATCTCTAAATGAA 728
?
? 264 CAGCTGACGACGACACAGCGCTGTACTACTGTGAGAGAGATTTAGATACAGTAA 323
? 729 CAGCTGACGACGACGACGCTGTACTACTGTGAGAGAGAT-----CAGAGCCT 782

```

RESULT 14

QY 324 TTTCCTCCGTTGGGTCGAGCAGGTATGAGCTCTGGGGCCAGGGACACGGTCAT 383
DB 783 GTTGGGTACTATATAGCCACTACTAGCTTTGGAGCTCTGGGGCAAGGACACCGTCAC 842
QY 384 CGTCTCTCA 393
DB 843 CGTCTCTCA 852

RESULT 15

US-09-194-164-15/c
Sequence 15, Application US/09194164
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.
Maitl, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 918 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-194-164-15

Query Match 58.8%; Score 231.2; DB 5; Length 918;

Best Local Similarity 78.6%; Pred. No. 6.2e-62;

Matches 291; Conservative 0; Mismatches 73; Indels 6; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGCCTTGGGGGTCCTGAGACTCTCTGTGCACG 83

DB 430 GGTGAGTCTGGGGAGGCGCTGTCAGCCTTGGGGGTCCTGAGACTCTCTGTGCACG 371

QY 84 CTCGTGATTCACCTTCAGTATAGCATGACATGGGTCGCGCAGAGGTCAGGAAGG 143

DB 370 CTCGTGATTCACCTTCAGTATAGCATGACATGGGTCGCGCAGAGGTCAGGAAGG 311

QY 144 GCTGAGTGGTCTCATCTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203

DB 310 GCTGAGTGGTCTCATCTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 251

QY 204 GAAGGGCCGATTACACCATCTCCAGAGACAGCCAAAGAACTACTATCTGCAATGAA 263
DB 250 GAAGGGCCGATTACACCATCTCCAGAGACAGCTTCCAGAAACAGGATCTCAATAATGAA 191
QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGATTTAGATACAGTAA 323
DB 190 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGATTTAGATACAGTAA 137
QY 324 TTTCCTCCGTTGGGTCGAGCAGGTATGAGCTCTGGGGCCAGGGACACGGTCAT 383
DB 136 GTTGGGTACTATATAGCCACTACTAGCTTTGGAGCTCTGGGGCAAGGACACCGTCAC 77
QY 384 CGTCTCTCA 393
DB 76 CGTCTCTCA 67

RESULT 16

US-10-031-722A-1
Sequence 1, Application US/10031722A

GENERAL INFORMATION:

APPLICANT: Medarex, Inc.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU.

FILE REFERENCE: MXI-160PC

CURRENT APPLICATION NUMBER: US/10/031,722A

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: USSN 60/146,313

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: USSN 60/188,539

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 372

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(372)

US-10-031-722A-1

Query Match 58.5%; Score 230; DB 6; Length 372;

Best Local Similarity 78.6%; Pred. No. 1.1e-61;

Matches 291; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

QY 24 GGTGAGTCTGGGGAGGCGCTGTCAGCCTTGGGGGTCCTGAGACTCTCTGTGCACG 83

DB 12 GTTGGAGTCTGGGGAGGCGCTGTCAGCCTTGGGGGTCCTGAGACTCTCTGTGCACG 71

QY 84 CTCGTGATTCACCTTCAGTATAGCATGACATGGGTCGCGCAGAGGTCAGGAAGG 143

DB 72 CTCGTGATTCACCTTCAGTATAGCATGACATGGGTCGCGCAGAGGTCAGGAAGG 131

QY 144 GCTGAGTGGTCTCATCTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 203

DB 132 GCTGAGTGGTCTCATCTAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA 191

QY 204 GAAGGGCCGATTACACCATCTCCAGAGACAGCCAAAGAACTACTATCTGCAATGAA 263

DB 192 GAAGGGCCGATTACACCATCTCCAGAGACAGCTTCCAGAAACAGGATCTCAATAATGAA 251

QY 264 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGATTTAGATACAGTAA 323

DB 232 CAGCCTGAGAGCCGAGACACGCGTGTACTACTGTGCGAGAGATTTAGATACAGTAA 309

QY 324 TTTCCTCCGTTGGGTCGAGCAGGTATGAGCTCTGGGGCCAGGGACACGGTCAT 383

DB 310 -----TCGGGGAATTAT 362

QY 384 CGTCTCTCA 393

DB 363 CGTCTCTCA 372

	RESULT	17	US-09-194-164-18/c	
	Sequence	18,	Application US/09194164	
	GENERAL INFORMATION:			
	APPLICANT:	Dan, Michael D		
		Mall, Pradiip K.		
		Kaplan, Howard A.		
	TITLE OF INVENTION:	ANALYSIS AND BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS		
	NUMBER OF SEQUENCES:	18		
	CORRESPONDENCE ADDRESS:			
	ADDRESS:	Mortenson & Foerster		
	STREET:	55 Page Mill Road		
	CITY:	Palo Alto		
	STATE:	CA		
	COUNTRY:	USA		
	ZIP:	94304-1018		
	COMPUTER READABLE FORM:			
	MEDIUM TYPE:	Floppy disk		
	COMPUTER:	IBM PC compatible		
	OPERATING SYSTEM:	PC-DOS/MS-DOS		
	SOFTWARE:	Patentin Release #1.0, Version #1.30		
	CURRENT APPLICATION DATA:			
	APPLICATION NUMBER:	US/09/194,164		
	FILING DATE:	09-Apr-1999		
	CLASSIFICATION:	<Unknown>		
	PRIOR APPLICATION DATA:			
	APPLICATION NUMBER:	US/08/657,449		
	FILING DATE:	<Unknown>		
	ATTORNEY/AGENT INFORMATION:			
	NAME:	Lehnhardt, Susan K.		
	REGISTRATION NUMBER:	33,943		
	REFERENCE/DOCKET NUMBER:	31608-20001.00		
	TELECOMMUNICATION INFORMATION:			
	TELEPHONE:	(415) 813-5600		
	TELEFAX:	(415) 494-0792		
	TELEX:	706141		
	INFORMATION FOR SEQ ID NO: 18:			
	SEQUENCE CHARACTERISTICS:			
	LENGTH:	867 base pairs		
	TYPE:	nucleic acid		
	STRANDEDNESS:	single		
	TOPOLOGY:	linear		
	SEQUENCE DESCRIPTION:	SEQ ID NO: 18:		
	US-09-194-164-18			
	Query Match	58.4%;	Score 229.6;	DR 5; Length 867;
	Best Local Similarity	78.4%;	Pred. No. 1.9e+61;	
	Matches 290;	Conservative	0; Mismatches 74;	Indels 6; Gaps 1;
OY	24	GGTGAGTCTGGGGAGCGCCGTGTCACAGCCTGGGGGTCCCTGTGACTCTCTGTGCAGC	83	
DB	430	GGTGAGATCTGGSGAGCGCTGGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGCAGC	371	
OY	84	CTCTGATTCACCTTCAGTAGCTACATACAGCATGCTGGGTCCGCCAGGAGTCCAGGAAGG	143	
DB	370	CTCTGGATTCCTCCCTTCAGAACTTTGCTATGCACTGGGGTCCGCCAGGCTTAGCAAGG	311	
OY	144	GCTGAGCTGGGTCTCATCTCATTAAGTAATAGTAATACTTACATATACATACGAGAGCGAGT	203	
DB	310	GCTGAGTGGGTGGCACTTATATCATATGATGAGAAGCACTAATATCTACGAGACTCCGT	251	
OY	204	GAAGGCGCATTCACCATCTCCAGAGACAAGCCAGAAGAACCTACCTTCTGCAAATGAA	263	
DB	250	GAAGGCGCATTCACCATCTCCAGAGACTTCGAAGAACCGGATATCTAAAAATGAA	191	
OY	264	CAGCCTGAGACCGAGCACAGCGGTGTACTACTGTCGAGAGATTTAGATTACAGTAA	323	
DB	190	CAGCCTGAGACTGGAGACAGCGCTGTCTATTACTGTGGAGAGAT-----CAGAGCCT	137	

OY		324	TTCCTCCGTTGGGTTCGAGCGACGCATATGACGCTTGCGGCCAAGGAAACCAGCCTCAT	383
Db		136	GTTGGGACTATGACCACTTACAGGATTGGTGCTGTGGGAAGAAGAACACCGCTCAC	77
OY		384	CGETCCTCA 393 	
Db		76	CGTCTCCTCA 67	
RESULT 18				
US-09-849-390-121				
; Sequence 121, Application US/09849390				
; GENERAL INFORMATION:				
APPLICANT : Northwestern University				
APPLICANT : ROWLEY, Anne				
APPLICANT : BAKER, Susan				
APPLICANT : SHUDMAN, Stanford				
TITLE OF INVENTION: Methods and Compositions Related to Kawasaki Disease				
FILE REFERENCE: 0290-4682 (US/09/849,390)				
CURRENT APPLICATION NUMBER: US/01-05-24				
PRIOR FILING DATE: 2000-05-04				
NUMBER OF SEQ ID NOS: 121				
SOFTWARE: PatentIn version 3.0				
SEQ ID NO: 121				
LENGTH: 360				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-849-390-121				
Query Match 57.8% ; Score 227 ; DB 5 ; Length 360;				
Best Local Similarity 87.6% ; Pred. No. 9, 2e+61 ;				
Matches 24 ; Conservative 0 ; Mismatches 35 ; Indels 0 ; Gaps 0				
OY		24	GGTGAATCTCGGGGAGCGCTGTGTCAAAGCCTGGGGGGTCCCCTTAGACTCTCCCTGTGACG 83	
Db		12	GGTGAATCTCGGGGGGGCTGTGTGTCAAAGCCTGGAGGGCTCCCTAGACTCTCTGTGACG 71	
OY		84	CTCTGGATTAACCTTCACTAGTACTATATAGATGACACTGGGCTCCGACGGSTCCAGSAAAGG 143	
Db		72	CTCTGGATTAACCTTCACTAGTACTATATAGTACTAGTGTGGTTCCGCGAGGCTCCAGGAAAGG 131	
OY		144	GCTGAGTGGGTCTATCCATCTTATAGTATACTTACAATATATAGAGAGAGACGAGT 203	
Db		132	A CTGAGAGCGCTTCATATATACATAGAGAGAGTATTAACCAAGTACGAGACTCTGT 191	
OY		204	GAAGGCGCATTAACCATCTCCAAGACAAAGCCCAAGAACTCACTGATCTGCAAAATGAA 263	
Db		192	GAAGGCGCATTAACCATCTCCAAGACAAAGCCCAAGAACTCACTGATCTGCAAAATGAG 251	
OY		264	CAGCTGAGAGCCGACACAGCGCTGTACTACATCTGSCGGA 306	
Db		252	CAGCTGAGAGCCGACACAGCGCTGTATATTA TGTGTGCGAGA 294	
RESULT 19				
US-10-031-722A-5				
; Sequence 5, Application US/10031722A				
; GENERAL INFORMATION:				
APPLICANT : Medarex, Inc.				
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HBZ2/NEU				
FILE REFERENCE: MXI-10PDC				
CURRENT APPLICATION NUMBER: US/10/031,722A				
CURRENT FILING DATE: 2000-07-25				
PRIOR APPLICATION NUMBER: USSN 60/146,313				
PRIOR FILING DATE: 1999-07-29				
PRIOR APPLICATION NUMBER: USSN 60/188,539				
PRIOR FILING DATE: 1999-03-10				
NUMBER OF SEQ ID NOS: 13				
SOFTWARE: PatentIn Ver. 2.0				
SEQ ID NO 5				

LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(366)
US-10-031-722a-5

Query Match 57.5%; Score 226; DB 6; Length 366;
Best Local Similarity 78.4%; Pred. No. 1.9e-60;
Matches 290; Conservative 0; Mismatches 65; Indels 15; Gaps 1;

OY 24 GGTGAGTCTGGGGAGGCGCTGTCACGCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTCACGCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 71
OY 84 CTCGTGATTCACTTCACTATAGCATGACATGCGGTCGCGCCAGGGTCCAGGAAAGG 143
DB 72 GTCGTGATTCACTTCACTATAGCATGACATGCGGTCGCGCCAGGGTCCAGGAAAGG 131
OY 144 GCTGAGTGGGTCTCATCTTATAGTAATATATATATATATATATATATATATATATAT 203
DB 132 GCTGAGTGGGTCTCATCTTATAGTAATATATATATATATATATATATATATATATAT 191
OY 204 GAAGGCCGATTCACTATCCAGACACGCGCAAGACTCATGTATCTGCAATGAA 263
DB 192 GAAGGCCGATTCACTATCCAGACACGCGCTGATCTGCAATGAA 251
OY 264 CAGCTGAGACCGGACGACGCGCTGATCTGCGAGAGATTCTAGTACAGTAA 323
DB 252 CAGCTGAGACCGGACGACGCGCTGATCTGCGAGAACTATGTTGGGAG 311
OY 324 TTTCTCCGTTGGTTCGAGGAGGATGAGGCTGGGGGCAAGGACACGCTCAT 383
DB 312 TT-----ATTTAACTACTTGTGCGGCGCAGGGAACCTGTGCAC 356
OY 384 GGTCTCTCA 393
DB 357 GGTCTCTCA 366

RESULT 20
PCT-US03-25161-17
Sequence 17, Application PC/TUS0325161
GENERAL INFORMATION:
APPLICANT: Abgenix, Inc.
APPLICANT: Roskos, Lorin
APPLICANT: Folz, Ian
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
FILE REFERENCE: ABGENIX.092VPC
CURRENT APPLICATION NUMBER: PCT/US03/25161
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 352
TYPE: DNA
ORGANISM: Homosapien
PCT-US03-25161-17

Query Match 57.5%; Score 225.8; DB 1; Length 352;
Best Local Similarity 87.0%; Pred. No. 2.2e-60;
Matches 248; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY 24 GGTGAGTCTGGGGAGGCGCTGTCACGCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 83
DB 12 GGTGAGTCTGGGGAGGCGCTGTCACGCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 71
OY 84 CTCGTGATTCACTTCACTATAGCATGACATGCGGTCGCGCCAGGGTCCAGGAAAGG 143
DB 72 CTCGTGATTCACTTCACTATAGCATGACATGCGGTCGCGCCAGGGTCCAGGAAAGG 131

OY 144 GCTGAGTGGGTCTCATCTTATAGTAATATATATATATATATATATATATATATATAT 203
DB 132 GCTGAGTGGGTCTCATCTTATAGTAATATATATATATATATATATATATATATATAT 191
OY 204 GAAGGCCGATTCACTATCCAGACACGCGCAAGACTCATGTATCTGCAATGAA 263
DB 192 GAAGGCCGATTCACTATCCAGACACGCGCTGATCTGCAATGAA 251
OY 264 CAGCTGAGACCGGACGACGCGCTGATCTGCGAGAGATTCTAGTACAGTAA 308
DB 252 CAGCTGAGACCGGACGACGCGCTGATCTGCGAGAGATTCTAGTACAGTAA 296

Search completed: September 24, 2003, 05:54:52
Job time : 866 secs

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